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OM nucleic - nucleic search, using sw model

Run on: July 22, 2005, 00:57:09 ; Search time 433 Seconds
(without alignments)

Million cell updates/sec 1722.604

Title: US-10-764-581-17

Perfect score: 126

Sequence: 1 catagacttagggggccatggggaaatgtatggaaacatgtatggaa 126

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_1.6Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query	Match	Length	DB	ID	Description
1	126	100.0	126	10	ACC43720		Ac43720 Nucleotid
c 2	30.5	4653	4	ABJ05742			Ab105742 Drosophil
c 3	36.4	28.9	2121	6	ABJ0526		Abq70526 Listeria
c 4	36	28.6	6112	4	ABJ36298		Aa136297 Human mus
c 5	36	28.6	6112	4	ABJ36297		Abx59285 cDNA enco
c 6	36	28.6	6112	8	ABX59285		Abx59286 cDNA enco
c 7	36	28.6	6112	8	ABX59286		Adj30035 Human mus
c 8	36	28.6	6112	12	ADJ30035		Adj30036 Human mus
c 9	36	28.6	6112	12	ADJ30036		Continuation (17 o
c 10	36	28.6	110000	6	ABA03041_16		Abq7108 Human ang
c 11	35.6	28.3	5237	6	ABA03041_16		Ada02987 Mouse Cd2
c 12	35.4	28.1	27587	9	ADA02987		Abd72725 Mouse Cd2
c 13	35.4	28.1	27587	10	ADB72725		Adc85467 Mouse Cd2
c 14	35.4	28.1	27587	10	ADC85467		Adm74582 Murine ca
c 15	35.4	28.1	27587	12	ADM74582		Continuation (17 o
c 16	34.8	27.6	110000	6	ABQ69245_16		Abq80552 Human Can
c 17	34.8	27.6	110000	6	ABQ69245_16		Aaf74632 Bacillus
c 18	34.4	27.3	7450	6	ABK28131		Abq80552 Human Can
c 19	34.4	27.3	237961	6	ABQ80552		Abq80552 Human Can
c 20	34.2	27.1	906	4	AAF74632		

SEARCH

ALIGMENTS

CC synthesis from a DNA template comprising a promoter with at least one UP
 CC element, and recovering the synthesized RNA or polypeptide. The method is
 CC useful for synthesizing RNAs or polypeptides from a DNA template. The RNA
 CC produced from the method is useful as an mRNA for in vitro protein
 CC synthesis, as hybridization probes in diagnostic assays, as substrates
 CC for analysing processing reactions or RNA splicing, and for the
 CC production of specific proteins of interest, such as antigens for
 CC vaccines. (Updated on 27-OCT-2003 to standardise OS field)

XX Sequence 126 BP; 49 A; 14 C; 28 G; 35 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 126; DB 10; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db Query 1 CATAAGCTTAGGGAGGGCAGAAAAATCTCGAAATTATTACATTGATT 60
 Db 1 CATAAGCTTAGGGAGGGCAGAAAAATCTCGAAATTATTACATTGATT 60
 Qy 61 TTATTTTATACAGTATTATGAAACTACATGAGGATACAGTATTATGAACT 120
 Db 61 TTATTTTATACAGTATTATGAAACTACATGAGGATACAGTATTATGAACT 120
 Qy 121 ATGAAAC 126
 Db 121 ATGAAAC 126

RESULT 2
 ABL05742/C
 ID ABL05742 standard; cDNA; 4663 BP.
 AC ABL05742;
 XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polymucleotide SEQ ID NO 11708.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 KW Drosophila melanogaster.
 OS WO200171042-A2.
 XX PD 27-SBP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-01916375.
 PR 11-JUL-2000; 2000US-0061-150.
 PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;
 DR WPI; 2001-656860/75.
 DR P-PSDB; ABB61639.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX Claim 1; SEQ ID NO 11708; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL1616-ABL3051), expressed DNA
 CC sequences (ABL01840-ABL1675) and the encoded proteins (ABBS7737-
 ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 4663 BP; 1252 A; 1104 C; 1094 G; 1213 T; 0 U; 0 Other;
 SQ Query Match 30.5%; Score 38.4; DB 4; Length 4663;
 Best Local Similarity 62.5%; Pred. No. 7.6;
 Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 Qy 27 AAATCTCTGAAATTATTAAATACATTTGATTTTACAGTATTATGAG 86
 Db 2341 AAATCTGAAAGGTTTATACCCACATAAACATTGTATTAAATGAGCTT 2282
 Qy 87 AACTACATGAGGATACGGTGGACATGAT 122
 Db 2281 TACTACATGAGGCCATCCATGATATGTACATGAT 2246
 RESULT 3
 ABQ70526/c
 ID ABQ70526 standard; DNA; 2121 BP.
 XX AC ABQ70526;
 XX DT 29-AUG-2003 (revised)
 DT 29-AUG-2002 (first entry)
 XX DE Listeria monocytogenes 4b contig DNA sequence #468.
 XX KW Antibacterial; Listeria; food contamination; mutational analysis;
 KW infection; ds.
 OS Listeria monocytogenes ATCC 19115.
 XX OS Listeria monocytogenes ATCC 19115.
 XX PN WO200228891-A2.
 XX PD 11-APR-2002.
 XX PP 04-OCT-2001; 2001WO-FR003061.
 XX PR 04-OCT-2000; 2000FR-00012697.
 XX PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA Kunst F, Glasner P;
 PI Kunst F, Glasner P;
 XX DR WPI; 2002-332479/37.
 XX PT New genomic sequences from Listeria species, useful for detection,
 PT treatment and prevention of infection, also related polypeptides,
 PT antibodies and modulators.
 XX PS Claim 14; SEQ ID NO 3339; 180pp; French.
 XX CC The present invention relates to nucleic acid sequences (ABQ67188-
 CC ABQ71212) from Listeria sp. The sequences are useful as probes and
 CC primers for identification and/or detection of Listeria (e.g. as
 CC contaminants in foods, or mutational analysis) and for analysis of gene
 CC expression. Proteins encoded by the nucleic acid sequences can be used to
 CC screen for compounds that modulate gene expression, replication and
 CC pathogenicity of Listeria (potential therapeutic agent), also for
 CC treating infections by Listeria, and are useful as immunogens in anti-
 CC Listeria vaccines. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated
 CC on 29-AUG-2003 to standardise OS field)
 XX Sequence 2121 BP; 581 A; 449 C; 365 G; 722 T; 0 U; 4 Other;
 SQ Query Match 28.9%; Score 36.4; DB 6; Length 2121;
 Best Local Similarity 59.8%; Pred. No. 21;
 Matches 61; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy	24	AAAATACTCCGAAATTAAATATACATTGATTATTATACAGTATTATAAT	83
Db	219	AAAATAGTTTAAATATTAAAAACATTGACATTAAATACATCATTATAAT	160
Qy	84	GAGAACTACATGAGGCAACGGGTAGGGGAAACATGTGAA	125
Db	159	GAAAATGTCATTTAACTTAAACGGACGGTAAAGGATCAA	118
RESULT 4			
	AAL36298/C	Human musculoskeletal system related polynucleotide SEQ ID NO 2663.	
ID	AAL36298	standard; DNA; 6112 BP.	
XX	XX		
AC	AC		
XX	XX		
DT	08-JAN-2002	(first entry)	
XX	XX		
DB	DB		
XX	XX		
KW	Cytostatic; immunosuppressive; nootropic; neuroprotective; anti-viral;		
KW	anti-allergic; hepatotropic; anti-diabetic; anti-inflammatory; antiulcer;		
KW	vulnerant; anticonvulsant; antibacterial; antifungal; anti-parasitic;		
KW	cardiary; gene therapy; cancer; immune disorder; cardiovascular disorder;		
KW	neurological disease; infection; human; secreted protein;		
KW	musculoskeletal system; ds.		
XX	XX		
OS	OS		
XX	XX		
PN	PN		
XX	XX		
PD	02-AUG-2001.		
XX	XX		
PF	17-JAN-2001; 2001WO-US001338.		
XX	XX		
PR	31-JAN-2000; 2000US-0179065P.		
PR	04-FEB-2000; 2000US-0180628P.		
PR	24-FEB-2000; 2000US-0184664P.		
PR	02-MAR-2000; 2000US-0189350P.		
PR	16-MAR-2000; 2000US-0189874P.		
PR	17-MAR-2000; 2000US-0190076P.		
PR	18-APR-2000; 2000US-0198123P.		
PR	19-MAY-2000; 2000US-0205515P.		
PR	07-JUN-2000; 2000US-0209467P.		
PR	28-JUN-2000; 2000US-0214886P.		
PR	30-JUN-2000; 2000US-0215135P.		
PR	07-JUL-2000; 2000US-0216647P.		
PR	07-JUL-2000; 2000US-0216880P.		
PR	11-JUL-2000; 2000US-0217487P.		
PR	11-JUL-2000; 2000US-0217496P.		
PR	14-JUL-2000; 2000US-0218290P.		
PR	26-JUL-2000; 2000US-0220963P.		
PR	26-JUL-2000; 2000US-0220964P.		
PR	14-AUG-2000; 2000US-0224510P.		
PR	14-AUG-2000; 2000US-0224519P.		
PR	14-AUG-2000; 2000US-0225213P.		
PR	14-AUG-2000; 2000US-0225214P.		
PR	14-AUG-2000; 2000US-0225266P.		
PR	14-AUG-2000; 2000US-0225267P.		
PR	14-AUG-2000; 2000US-0225270P.		
PR	22-AUG-2000; 2000US-0225447P.		
PR	22-AUG-2000; 2000US-0227182P.		
PR	23-AUG-2000; 2000US-0227009P.		
PR	30-AUG-2000; 2000US-0228924P.		
PR	01-SEP-2000; 2000US-0228928P.		
PR	01-SEP-2000; 2000US-0229345P.		

PR	01-SEP-2000	2000US-0229344P.
PR	01-SEP-2000	2000US-0229345P.
PR	05-SEP-2000	2000US-0229513P.
PR	05-SEP-2000	2000US-0229513P.
PR	06-SEP-2000	2000US-0230437P.
PR	06-SEP-2000	2000US-0230438P.
PR	08-SEP-2000	2000US-0231242P.
PR	08-SEP-2000	2000US-0231243P.
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PR	08-SEP-2000	2000US-0231414P.
PR	08-SEP-2000	2000US-0232080P.
PR	08-SEP-2000	2000US-0232081P.
PR	12-SEP-2000	2000US-0232397P.
PR	14-SEP-2000	2000US-0232398P.
PR	14-SEP-2000	2000US-0232399P.
PR	14-SEP-2000	2000US-0232400P.
PR	14-SEP-2000	2000US-0232401P.
PR	14-SEP-2000	2000US-0233063P.
PR	14-SEP-2000	2000US-0233064P.
PR	14-SEP-2000	2000US-0233065P.
PR	21-SEP-2000	2000US-0234223P.
PR	21-SEP-2000	2000US-0234224P.
PR	25-SEP-2000	2000US-0234937P.
PR	25-SEP-2000	2000US-0234938P.
PR	26-SEP-2000	2000US-0235484P.
PR	27-SEP-2000	2000US-0235834P.
PR	27-SEP-2000	2000US-0235836P.
PR	29-SEP-2000	2000US-0236327P.
PR	29-SEP-2000	2000US-0236337P.
PR	01-OCT-2000	2000US-0237034P.
PR	01-OCT-2000	2000US-0237040P.
PR	13-OCT-2000	2000US-0239935P.
PR	13-OCT-2000	2000US-0239937P.
PR	20-OCT-2000	2000US-0240960P.
PR	20-OCT-2000	2000US-0241212P.
PR	20-OCT-2000	2000US-0241785P.
PR	20-OCT-2000	2000US-0241806P.
PR	20-OCT-2000	2000US-0241877P.
PR	08-NOV-2000	2000US-0241808P.
PR	08-NOV-2000	2000US-0241809P.
PR	08-NOV-2000	2000US-0244676P.
PR	08-NOV-2000	2000US-0246417P.
PR	08-NOV-2000	2000US-0246512P.
PR	08-NOV-2000	2000US-0246513P.
PR	08-NOV-2000	2000US-0246514P.
PR	08-NOV-2000	2000US-0246515P.
PR	08-NOV-2000	2000US-0246526P.
PR	08-NOV-2000	2000US-0246527P.
PR	08-NOV-2000	2000US-0246528P.
PR	08-NOV-2000	2000US-0246532P.
PR	08-NOV-2000	2000US-0246609P.
PR	08-NOV-2000	2000US-0246610P.
PR	08-NOV-2000	2000US-0246611P.
PR	17-NOV-2000	2000US-0246613P.
PR	17-NOV-2000	2000US-0249208P.
PR	17-NOV-2000	2000US-0249209P.
PR	17-NOV-2000	2000US-0249210P.
PR	17-NOV-2000	2000US-0249211P.
PR	17-NOV-2000	2000US-0249212P.

PR	17-NOV-2000;	2000US-0249214P.	XX	AAL36297/C
PR	17-NOV-2000;	2000US-0249215P.	AC	AAL36297;
PR	17-NOV-2000;	2000US-0249216P.	XX	
PR	17-NOV-2000;	2000US-0249217P.	DT	08-JAN-2002 (first entry)
PR	17-NOV-2000;	2000US-0249218P.	XX	Human musculoskeletal system related polynucleotide SEQ ID NO 2662.
PR	17-NOV-2000;	2000US-0249244P.	DE	
PR	17-NOV-2000;	2000US-0249245P.	XX	
PR	17-NOV-2000;	2000US-0249264P.	XX	
PR	17-NOV-2000;	2000US-0249265P.	KW	Cytostatic; immunosuppressive; nocotropic; neuroprotective; antiviral;
PR	17-NOV-2000;	2000US-0249297P.	KW	antiallergic; hepatotoxic; antidiabetic; antiinflammatory; antulcer;
PR	05-DEC-2000;	2000US-0249399P.	KW	vulnery; anticonvulsant; antibacterial; antiparasitic;
PR	17-NOV-2000;	2000US-0249100P.	KW	cardian; gene therapy; cancer; immune disorder; cardiovascular disorder;
PR	01-DEC-2000;	2000US-0250165P.	KW	neurological disease; infection; human; secreted protein;
PR	05-DEC-2000;	2000US-0250191P.	KW	musculoskeletal system; ds.
PR	05-DEC-2000;	2000US-0251030P.	XX	
PR	05-DEC-2000;	2000US-025198P.	XX	
PR	05-DEC-2000;	2000US-0256719P.	OS	Homo sapiens.
PR	06-DEC-2000;	2000US-0251479P.	XX	
PR	08-DEC-2000;	2000US-025155P.	PN	WO200155367-A1.
PR	08-DEC-2000;	2000US-0251686P.	XX	
PR	08-DEC-2000;	2000US-025186P.	PD	02-AUG-2001.
PR	08-DEC-2000;	2000US-025189P.	XX	
PR	11-DEC-2000;	2000US-025190P.	PF	17-JAN-2001; 2000WO-US001338.
PR	05-JAN-2001;	2001US-0251967P.	XX	
PA	(HUMAN) HUMAN GENOME SCI INC.		XX	
XX	Rosen CA,	Barash SC,	Ruben SM;	
XX	WPI:	2001-451937/48.		
DR				
PT	Isolated polypeptide for treating, preventing and/ or prognosing			
PT	disorders related to the musculoskeletal system including musculoskeletal			
PT	cancers and also for testing and detection e.g. diagnosis.			
PS	Example 2: SEQ ID NO 2663; 781pp + Sequence Listing; English.			
XX	The invention relates to novel genes (AAL34669-AAL37666) and proteins			
CC	(ABB03087-ABB04109) associated with the musculoskeletal system useful for			
CC	preventing, treating or ameliorating medical conditions e.g. by protein			
CC	or gene therapy. The genes are isolated from a range of human tissues			
CC	disclosed in the specification. The nucleic acids, proteins, antibodies			
CC	and (ant)agonists are useful in the diagnosis, treatment and prevention			
CC	of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the			
CC	adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,			
CC	lung, or urogenital e.g. Addison's disease,			
CC	(b) immune disorders e.g. by protein			
CC	allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,			
CC	diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid			
CC	arthritis and ulcerative colitis; (c) cardiovascular disorders such as			
CC	myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.			
CC	cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,			
CC	bacterial, fungal and parasitic infections. Note: The sequence data for			
CC	this patent did not form part of the printed specification, but was			
CC	obtained in electronic format directly from WIPO at			
CC	ftp://wipo.int/pub/published_pct_sequences			
XX	Sequence 6112 BP; 1894 A; 905 C; 1243 G; 2070 T; 0 U; 0 Other;			
Query	Query Match 28.6%; Score 36; DB 4; Length 6112;			
Query	Best Local Similarity 62.0%; Pred. No. 29; Mismatches 57; Conservative 0;			
Db	18 GCAAGAAAAAAATCCCTCGAAATTATAATTATAATCATTTGATTTTATACAGTAT 77			
Db	2667 GCAAAAGAGACTACATTAACAGCACTAAATGGTATAATTGTGATAATGTACCTAT 2608			
Qy	78 TATAATGAAACTACATGGCTACGGCTACGGCTA 109			
Db	2607 TATTTTAAGAATTATATAATGAAATCTGATAA 2576			
RESULT	5			

PR 08-SEP-2000; 2000US-0232088P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231965P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234222P.
 PR 25-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235488P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235835P.
 PR 29-SEP-2000; 2000US-0236322P.
 PR 29-SEP-2000; 2000US-0236323P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239936P.
 PR 20-OCT-2000; 2000US-0236802P.
 PR 20-OCT-2000; 2000US-0236803P.
 PR 20-OCT-2000; 2000US-0236804P.
 PR 20-OCT-2000; 2000US-0241222P.
 PR 01-NOV-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
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 PR 08-NOV-2000; 2000US-0241809P.
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 PR 08-NOV-2000; 2000US-0241826P.
 PR 08-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246174P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
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 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246529P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249255P.
 PR 17-NOV-2000; 2000US-0249287P.
 PR 17-NOV-2000; 2000US-0249299P.

PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254077P.
 PR 05-JAN-2001; 2000US-0254678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PA
 PI Rosen CA, Barash SC, Ruben SM,
 XX DR WPI: 2001-451937/48.
 XX Isolated polypeptide for treating, preventing and/ or prognosing
 PT disorders related to the musculoskeletal system including musculoskeletal
 PR cancers and also for testing and detection e.g. diagnosis.
 XX
 Example 2; SEQ ID NO 2662; 781pp + Sequence Listing; English.
 XX
 The invention relates to novel genes (AAU34661-AAU37666) and proteins
 CC (AB01087-AB04109) associated with the musculoskeletal system useful for
 CC preventing, treating or ameliorating medical conditions e.g. by protein
 CC or gene therapy. The genes are isolated from a range of human tissues
 CC disclosed in the specification. The nucleic acids, proteins, antibodies
 CC and (ant)agonists are useful in the diagnosis, treatment and prevention
 CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, Gastrointestinal tract, liver,
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
 CC myocardial ischaemia and epilepsy; and (e) neurological diseases e.g.
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
 CC bacterial, fungal and parasitic infections. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX
 Sequence 6112 BP; 1894 A; 905 C; 1243 G; 2070 T; 0 U; 0 Other;
 SQ Score 36; DB 4; Length 6112;
 Best Local Similarity 62.0%; Pred. No. 29;
 Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 Qy 18 GCAAGGAAAAAATCTCTGAAAAATTAAATATACATTGATTATTATACAGTAT 77
 Db 2667 GAAAAAAAGCTACACTAAACGACTAAATGTATAATGTATAATGTATAATGCTCTAT 2608
 Qy 78 TATAATGAGAACTCATGTAGGCTATGGGTGA 109
 Db 2607 TATTAAAGAAATTATAATGTATACTGATA 2576

RESULT 6
 ABX59285/c
 ID ABX59285 standard; cDNA: 6112 BP.
 XX
 AC ABX59285;
 XX
 DT 26-FEB-2003 (First entry)
 XX
 CDNA encoding novel human musculoskeletal system antigen #1629.
 XX
 KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
 KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;

KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
 KW post-operative tissue repair; limb regeneration; neuronal growth;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW AIDS-related complex; chondrocyte growth; bone regeneration;
 KW periodontal regeneration; tissue transport; bone graft; skin aging;
 KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
 KW cell growth; organ transplant; cell differentiation; body height; weight;
 KW hair colour; eye colour; skin; percentage of adipose tissue;
 KW pigmentation; cosmetic surgery; metabolism; biorhythm; arrhythmic rhythm;
 KW depression; tendency for violence; pain; reproductive capability;
 KW hormone level; endocrine level; appetite; libido; memory; stress;
 KW storage capability; fat content; lipid content; protein content;
 KW carbohydrate content; vitamin content; cofactor content;
 KW nutritional component.

XX Homo sapiens.

PN US2002147140-A1.

XX PD 10-OCT-2002.

XX PF 17-JAN-2001; 2001US-0076487.

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-018052P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216547P.

PR 07-JUL-2000; 2000US-016880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-01829P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-022557P.

PR 22-AUG-2000; 2000US-0225758P.

PR 30-AUG-2000; 2000US-022668P.

PR 01-SEP-2000; 2000US-0228994P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 05-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229513P.

PR 21-SEP-2000; 2000US-0231413P.

PR 21-SEP-2000; 2000US-0234223P.

PR 25-SEP-2000; 2000US-0234274P.

PR 27-SEP-2000; 2000US-0234957P.

PR 29-SEP-2000; 2000US-0235834P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-023935P.

PR 20-OCT-2000; 2000US-024060P.

PR 20-OCT-2000; 2000US-0241785P.

PR 01-NOV-2000; 2000US-0244617P.

PR 17-NOV-2000; 2000US-0249299P.

PR 08-DEC-2000; 2000US-0251888P.

PR 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.
 PA (RUBEN/) RUBEN S M.
 PA (BARA/) BARASH S C.

XX PI Rosen CA, Ruben SM, Barash SC;

XX DR WPI; 2003-128199/12.

XX PT Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.

XX Disclosure; SEQ ID NO 2662; 321pp; English.

XX PS

XX CC The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid stimulates re-vascularization of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcerS; stimulates angiogenesis and limb regeneration; stimulates neuronal growth, can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian growth and differentiation of adipose tissue, pigment, size, and shape (e.g., skin, percentage of adipose tissue, pigment, size, and shape (e.g., cosmetic surgery)); modulates mammalian metabolism, changes mammal's metal state or physical state by influencing biorhythms, circadian rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional component. This sequence encodes a novel human musculoskeletal system antigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at ftp://seqdata.uspto.gov/sequence.html?DocID=20020147140

XX SQ Sequence 6112 BP; 1894 A; 905 C; 1243 G; 2070 T; 0 U; 0 Other;

XX SQ

Query Match 28 6%; Score 36; DB 8; Length 6112;

Best Local Similarity 62.0%; Pred. No. 29;

Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 18 GCAAGAAAAATCTCTGAAATTAAATACATTGATTATTTTATACAGTAT 77

Db 2667 GGAAAGAAAGAGTACACTAACAGCTAAATGATAATGTACCTAT 2608

Qy 78 TATAATGAGAACTCATGAGCATAGGCTGA 109

Db 2607 TATTATGAGATATAATGAACTGATAA 2576

RESULT 7
ABX59386/c

ID ABX59386 standard; cDNA; 6112 BP.

XX AC ABX59386;

DT 26-FEB-2003 (first entry)

DE CDNA encoding novel human musculoskeletal system antigen #1630.

Gene; ss; musculoskeletal system antigen; cancer; metastasis; re-vascularisation; thrombosis; arteriosclerosis; mineral content; cardiovascular condition; wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; AIDS-related complex; chondrocyte growth; bone regeneration; periodontal regeneration; tissue transplant; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight; hair colour; eye colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm; dopamine; tendency for violence; pain; reproductive capability; hormone level; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content; carbohydrate content; vitamin content; cofactor content; nutritional component.

PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
XX	(ROSE /)	ROSEN C A.
PA	(RUBE /)	RUBEN S M.
PA	(BARA /)	BARASH S C.
XX	Rosen CA,	Ruben SM,
PI	XX	Barash SC;
WPI;	2003-128199/12.	
XX	DR	Isolated nucleic acid molecules ;
XX	PT	associated polypeptides, useful ;
XX	PT	Disclosure; SEQ ID NO 2663; 321pp
PS	XX	

Disclosure; SEQ ID NO 2663; 321pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a sequence encoding a musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularization of ischaemic tissues associated with conditions such as thrombosis, arterioclerosis, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates hair and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammal's mental state or physical state by influencing biorhythms, circadian rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This sequence encodes a novel human musculoskeletal system antigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at <ftp://seqdata.uspto.gov/Sequence.html?DOCID=20020147140>

XX	SQ	Sequence 6112 BP; 1894 A; 905 C; 1243 G; 2070 T; 0 U; 0 Other;
Query Match	28.6%	Score 36; DB 8; Length 6112;
Best Local Similarity	62.0%	Pred. No. 29;
Matches	57;	Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Qy	18	GCAAGAAAAAACTCTCGAAATTATAATTGATTATTGATTATTATAACAGTAT 77
Db	2667	GGAAAGAAGGTACATAACGCTAAATGGATTAATTTGATAAATGTACCTTAT 2608
Qy	78	TATAATGAGAACTACTACGAGGCAATCGGTGA 109
Db	2607	TATTAAAGATTATAATGATACTGTATAA 2576

Gene; ss; muscular	re-vascularisation
cardiovascular	cell
post-operative	cell
AIDS-related	cell
neurodegenerati	cell
periodontal reg	cell
keratinocyte gro	cell
cell growth; org	cell
hair colour; eye	cell
depression; tend	cell
hormone level; e	cell
storage capabili	cell
carbohydrate coo	cell
nutritional comp	cell
Homo sapiens.	
US2002147140-A1	
10-OCT-2002.	
17-JAN-2001; 200	
31-JAN-2000; 200	
04-FEB-2000; 200	
28-JUN-2000; 200	
07-JUL-2000; 200	
07-JUL-2000; 200	
11-JUL-2000; 200	
11-JUL-2000; 200	
14-JUL-2000; 200	
26-JUL-2000; 200	
26-JUL-2000; 200	
14-AUG-2000; 200	
22-AUG-2000; 200	
30-AUG-2000; 200	
01-SEP-2000; 200	
05-SEP-2000; 200	
08-SEP-2000; 200	
21-SEP-2000; 200	
21-SEP-2000; 200	
25-SEP-2000; 200	
27-SEP-2000; 200	
29-SEP-2000; 200	
29-SEP-2000; 200	
02-OCT-2000; 200	
13-OCT-2000; 200	
20-OCT-2000; 200	
20-OCT-2000; 200	
01-NOV-2000; 200	
17-NOV-2000; 200	

DT 20-MAY-2004 (first entry)

XX Human musculoskeletal system-associated genomic DNA - SEQ ID 2662.

DE XX musculoskeletal system; cytosatic; osteopathic; cancer; osteoporosis;

KW gene therapy; vaccine; human; ds.

XX Homo sapiens.

XX US2004009488-A1.

PD 15-JAN-2004.

XX 13-SEP-2002; 2002US-00242515.

XX PR 14-SEP-2000; 2000US-0231064P.

PR 14-SEP-2000; 2000US-0231065P.

PR 21-SEP-2000; 2000US-0231223P.

PR 21-SEP-2000; 2000US-0231274P.

PR 25-SEP-2000; 2000US-0231997P.

PR 25-SEP-2000; 2000US-0231998P.

PR 26-SEP-2000; 2000US-0231484P.

PR 27-SEP-2000; 2000US-0231834P.

PR 27-SEP-2000; 2000US-0231836P.

PR 29-SEP-2000; 2000US-0231327P.

PR 29-SEP-2000; 2000US-0231367P.

PR 29-SEP-2000; 2000US-0231368P.

PR 29-SEP-2000; 2000US-0231369P.

PR 02-OCT-2000; 2000US-0231370P.

PR 02-OCT-2000; 2000US-0231002P.

PR 02-OCT-2000; 2000US-0231037P.

PR 02-OCT-2000; 2000US-0231038P.

PR 02-OCT-2000; 2000US-0231039P.

PR 02-OCT-2000; 2000US-0231040P.

PR 13-OCT-2000; 2000US-0231935P.

PR 13-OCT-2000; 2000US-0231937P.

PR 20-OCT-2000; 2000US-02419960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0241617P.

PR 08-NOV-2000; 2000US-0241747P.

PR 08-NOV-2000; 2000US-024175P.

PR 08-NOV-2000; 2000US-024176P.

PR 08-NOV-2000; 2000US-0241809P.

PR 08-NOV-2000; 2000US-0241826P.

PR 08-NOV-2000; 2000US-0241877P.

PR 08-NOV-2000; 2000US-0241878P.

PR 08-NOV-2000; 2000US-0241523P.

PR 08-NOV-2000; 2000US-0241524P.

PR 08-NOV-2000; 2000US-0241525P.

PR 08-NOV-2000; 2000US-0241526P.

PR 08-NOV-2000; 2000US-0241527P.

PR 08-NOV-2000; 2000US-0241528P.

PR 08-NOV-2000; 2000US-0241532P.

PR 08-NOV-2000; 2000US-0241609P.

PR 08-NOV-2000; 2000US-0241610P.

PR 08-NOV-2000; 2000US-0241611P.

PR 08-NOV-2000; 2000US-0241613P.

PR 17-NOV-2000; 2000US-0241207P.

PR 17-NOV-2000; 2000US-0241213P.

PR 17-NOV-2000; 2000US-0241214P.

PR 17-NOV-2000; 2000US-0241245P.

PR 17-NOV-2000; 2000US-0241264P.

PR 17-NOV-2000; 2000US-0241265P.

PR 17-NOV-2000; 2000US-024127P.

PR 17-NOV-2000; 2000US-0241212P.

PR 17-NOV-2000; 2000US-0241213P.

PR 01-DEC-2000; 2000US-025160P.

PR 01-DEC-2000; 2000US-0251391P.

PR 05-DEC-2000; 2000US-0251030P.

PR 05-DEC-2000; 2000US-0251988P.

PR 05-DEC-2000; 2000US-0251719P.

PR 06-DEC-2000; 2000US-0251479P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251863P.
 PR 08-DEC-2000; 2000US-0251983P.
 PR 08-DEC-2000; 2000US-0251993P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2000US-0259670P.
 PR 17-JAN-2001; 2000US-00764877.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM, Barash SC;
 XX WPI; 2004-090458/09.
 DR XX Disclosure; SEQ ID NO 2662; 289pp; English.
 PS XX
 PT The invention relates to a novel isolated musculoskeletal system-associated nucleic acid molecule. The nucleic acid of the invention demonstrates cytosstatic and osteoplastic activities and may be useful for preventing, treating or ameliorating a medical condition e.g., cancer of the musculoskeletal tissues or osteoporosis.
 XX CC The invention relates to a novel isolated musculoskeletal system-associated nucleic acid molecule. The nucleic acid of the invention demonstrates cytosstatic and osteoplastic activities and may be useful for preparing a medicament for preventing, treating or ameliorating a medical condition such as cancer of the musculoskeletal tissues or osteoporosis, possibly via gene therapy or vaccine production. The current sequence is that of the human musculoskeletal system-associated genomic DNA of the invention. The current sequence is not shown within the specification because it is available on the USPTO web site
 CC <http://seqdata.uspto.gov/sequence.html?DocID=20040009488>.
 XX SQ Sequence 6112 BP; 1894 A; 905 C; 1243 G; 2070 T; 0 U; 0 Other;
 XX Best Local Similarity 28.6%; Score 36; DB 12; Length 6112;
 Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 Qy 18 GCGAGAARAAATCCTCGAAATTATAAATACATTGATTATTATAACAGTAT 77
 Db 2667 GGAARAAAGAGTACACTAACAGACTAAATGGATATAATGTTATAAATGCTCAT 2608
 Qy 78 TATAATGAGAACTACATGAGGCCATACGGGTGA 109
 Db 2667 TATTTAAGAAATTATAATGATACTGATAA 2576

Query Match
 Best Local Similarity 62.0%; Pred. No. 29;
 Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

XX RESULT 9
 ADJ30036/c
 ID ADJ30036 standard; DNA; 6112 BP.
 XX AC ADJ30036;
 XX DT 20-MAY-2004 (first entry)
 XX OS Homo sapiens.
 XX PN US2004009488-A1.
 XX PD 15-JAN-2004.
 XX PF 13-SEP-2002; 2002US-00242515.
 XX DB Human musculoskeletal system-associated genomic DNA - SEQ ID 2663.
 XX KW musculoskeletal system; cytosstatic; osteopathic; cancer; osteoporosis; gene therapy; vaccine; human; ds.
 XX PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186355P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-019076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217486P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 14-JUL-2000; 2000US-0218293P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225216P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225271P.
 PR 14-AUG-2000; 2000US-0225272P.
 PR 14-AUG-2000; 2000US-0225273P.
 PR 14-AUG-2000; 2000US-0225274P.
 PR 14-AUG-2000; 2000US-0225275P.
 PR 14-AUG-2000; 2000US-022578P.
 PR 14-AUG-2000; 2000US-022579P.
 PR 18-AUG-2000; 2000US-0226219P.
 PR 22-AUG-2000; 2000US-0226631P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0228287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231989P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 14-SEP-2000; 2000US-0233299P.
 PR 14-SEP-2000; 2000US-0234233P.
 PR 25-SEP-2000; 2000US-0234240P.
 PR 25-SEP-2000; 2000US-0233201P.
 PR 26-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-02333064P.
 PR 27-SEP-2000; 2000US-0233238P.
 PR 27-SEP-2000; 2000US-0234224P.
 PR 29-SEP-2000; 2000US-0234937P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236310P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.

ABQ67108/C
ID ABQ67108 standard; DNA; 5237 BP.
XX
AC ABQ67108;
XX
DT 28-AUG-2002 (first entry)
XX
Human angiogenesis associated polynucleotide SEQ ID NO 138.
XX Human; angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antiarthritic; antidiabetic; antipsoriatic; antiarteriosclerotic; ds.
XX OS Homo sapiens.
XX WO200246454-A2.
PN XX
XX
PD 13-JUN-2002.
PP 06-DEC-2001; 2001WO-EP014340.
PR 06-DEC-2000; 2000DE-01061338.
XX (EPIC) EPIGENOMICS AG.
XX
PT Schacht O;
XX WPI; 2002-500450/53.
DR XX
PT New nucleic acid fragments from chemically treated angiogenesis-associated genes useful for determining methylation status, e.g. in diagnosis or treatment of cancer.
XX Claim 1; SEQ ID NO 138; 41pp + Sequence Listing; German.
PS The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ671-ABQ6718) or their complements (I), also related oligomers, are used to evaluate the methylation status and/or single nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences
XX Sequence 5237 BP; 1086 A; 75 C; 1422 G; 2654 T; 0 U; 0 Other;
SQ Query Match 28.3%; Score 35.6; DB 6; Length 5237;
Best Local Similarity 67.6%; Pred. No. 35; Mismatches 24; Indels 0; Gaps 0;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21 AGAAAAAAATCCCTCGAAAATTAAATTAAATACATTGATTATTACAGTATTAT 80
Db 3883 AAATTAATTAATCCAAAAATCTTAAATTAAATTAAATAATAC 3824
Qy 81 ATGAGAACATCAT 94
Db 3823 AAAAACATCATCGT 3810
SQ Sequence 27587 BP; 7952 A; 5475 C; 5626 G; 8534 T; 0 U; 0 Other;
Query Match 28.1%; Score 35.4; DB 9; Length 27587;
Best Local Similarity 63.5%; Pred. No. 45;
Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 33 TCGAAATTATTAATAAATAATACATTGATTATTACAGTATTATAATGAGAACTAC 92
Db 7439 TCAAAACTATATAATATATTATTTCTTCCTTACATGACTGGAACTGC 7498
Qy 93 ATGAGAACATCCGGTGGGGAAC 117
Db 7499 CCAAGGAATTATGTGATGAAATC 7523
SQ RESULT 12
AD02387 ID AD02387 standard; DNA; 27587 BP.
XX AC AD02387;
XX DT 06-NOV-2003 (first entry)
XX

XX
PS Claim 1; SEQ ID NO 253; 29pp; English.

CC The invention relates to new recombinant nucleic acids. The invention
CC also relates to a host cell comprising a recombinant nucleic acid or
CC expression vector, an expression vector comprising a recombinant nucleic
CC acid, a recombinant protein, a method of screening for drug candidates, a
CC method of screening for a bioactive agent capable of binding to a
CC carcinoma associated protein (CAP) encoded by a nucleotide sequence, a
CC method of screening for a bioactive agent capable of modulating the
CC activity of a CAP, a method of evaluating the effect of a candidate
CC carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting
CC the activity of a CAP, a method of treating carcinomas, a method of
CC neutralising the effect of a CAP and a method of diagnosing carcinoma or
CC propensity to carcinoma. A method of evaluating the effect of a candidate
CC carcinoma drug comprises administering the drug to a patient, removing a
CC cell sample from the patient and determining alterations in the
CC expression or activation of a gene comprising the nucleotide sequence. A
CC method of diagnosing carcinoma comprises determining the expression of
CC one or more genes comprising the nucleic acid sequence in a first tissue
CC type of a first individual and comparing the expression of the gene from
CC a second normal tissue type from the first individual or a second
CC unaffected individual, where a difference in the expression indicates
CC that the first individual has carcinoma. A method of inhibiting the
CC activity of a CAP comprises binding an inhibitor to the CAP. Treating
CC carcinomas comprises administering to a patient an inhibitor of CAP.
CC Neutralising the effect of a CAP comprises contacting an agent specific
CC for the CAP. The polypeptide specifically binds to the protein encoded by
CC the nucleic acid. It comprises an antibody that specifically binds to the
CC protein encoded by the nucleic acid. The nucleic acids are useful for
CC preparing a composition for diagnosing or treating carcinoma e.g.,
CC leukaemia or lymphoma. This sequence represents a murine carcinoma
CC associated (CA) nucleic acid of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.

XX Sequence 27587 BP; 7952 A; 5475 C; 5626 G; 8534 T; 0 U; 0 Other;

Query Match 28.1% Score 35.4; DB 12; Length 27587;
Best Local Similarity 63.5%; Pred. No. 45;
Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 33 TCGRAAATTATTAATATACATTGATTATTATACAGTATTATAATGAGAACTAC 92
Db 7439 TCAAAACTATATAATATAATATTTTTCTCCCTACTAGCTGGAACTGC 7498
Qy 93 ATGAGGCCATACGGTGAGGGGAAAC 117
Db 7499 CCPAGGAAATTCAATGTGTTGGAAATC 7523

Search completed: July 22, 2005, 07:14:49
Job time : 440 sec

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Run on:	July 22, 2005, 01:04:54 ;	Search time 1882 Seconds (without alignments)	
Title:	US-10-764-581-17	3244.079 Million cell updates/sec	
Perfect score:	126		
Sequence:	1 catagacttagggggggca.....tgaggggggaaacatgtatggaa 126		
Scoring table:	IDENTITY_NUC		
Gapop 10-0 , Gapext 1.0			
Searched:	4708233 seqs, 24227607955 residues		
Total number of hits satisfying chosen parameters:	9416466		
Minimum DB seq length: 0			
Maximum DB seq length: 2000000000			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Listing First 45 summaries			
Database :	GenMbl:*		
	1: gb_ba:*		
	2: gb_htg:*		
	3: gb_in:*		
	4: gb_om:*		
	5: gb_ov:*		
	6: gb_pac:*		
	7: gb_ph:*		
	8: gb_pl:*		
	9: gb_pr:*		
	10: gb_ro:*		
	11: gb_srs:*		
	12: gb_sy:*		
	13: gb_un:*		
	14: gb_yi:*		
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
c 1	40.4	32.1 294250 1 AP001517	AP001517 Bacillus BX936455 Zebrafish BX957289 Danio rer
c 2	39.2	31.1 123705 5	Continuation (6 of AP432229 Drosophil
c 3	39.2	31.1 152061 2	AP432229 Drosophil
c 4	38.8	30.8 110000 2	CQ578096 Sequence
c 5	38.4	30.5 2307 3	Ac018035 Drosophil
c 6	38.4	30.5 4663 6	Continuation (14 o
c 7	38.4	30.5 41909 2	Continuation (13 o
c 8	38.4	30.5 51552 2	AC007624 Drosophil
c 9	38.4	30.5 110000 2	AC007593 Drosophil
c 10	38.4	30.5 167062 2	AE003789 Drosophil
c 11	38.4	30.5 173702 3	AE003789 Drosophil
c 12	38.4	30.5 333276 3	AL157831 Human DNA
c 13	37.8	30.0 176577 9	AC095039 Rattus no
c 14	37.6	29.8 245135 2	BX640454 Zebrafish
c 15	37.4	29.7 165038 5	AE017011 Bacillus
c 16	37.2	29.5 302422 1	AL929356 Plasmid
c 17	37.2	29.5 335050 3	Continuation (22 o
c 18	37	29.4 110000 8	CR382129_21
c 19	37	29.4 110000 8	Continuation (23 o

JOURNAL MEDLINE PUBMED	protein gene clusters from alkaliphilic <i>Bacillus</i> sp. strain C-125 99009008 10192928	CDS
REFERENCE 6	Authors Takami, H., Masui, N., Nakasone, K. and Horikoshi, K. Title Replication origin region of the chromosome of alkaliphilic <i>Bacillus halodurans</i> C-125 <i>Bacillus</i> Biotechnol. Biochem. 63 (2), 452-455 (1999)	unknown
JOURNAL MEDLINE PUBMED	Authors Takami, H., Takaki, Y., Nakasone, K., Sakiyama, T., Maeno, G., Hirama, C., Fuji, F. and Masui, N. Title Genetic analysis of the chromosome of alkaliphilic <i>Bacillus halodurans</i> C-125 Extremophiles 3 (3), 227-233 (1999)	gene CDS
REFERENCE 8	Authors Takami, H. and Horikoshi, K. Title Analysis of the genome of an alkaliphilic <i>Bacillus</i> strain from an industrial point of view Extremophiles 4 (2), 99-108 (2000)	gene CDS
JOURNAL MEDLINE PUBMED	Authors Nakasone, K., Masui, N., Takaki, Y., Sasaki, R., Maeno, G., Sakiyama, T., Hirama, C., Fuji, F. and Takami, H. Title Characterization and comparative study of the <i>rrn</i> operons of alkaliphilic <i>Bacillus halodurans</i> C-125 Extremophiles 4 (4), 209-214 (2000)	gene CDS
REFERENCE 10	Authors Takami, H., Nakasone, K., Takaki, Y., Maeno, G., Sasaki, R., Masui, N., Horikoshi, K. Title Complete genome sequence of the alkaliphilic bacterium <i>Bacillus halodurans</i> and genomic sequence comparison with <i>Bacillus subtilis</i> Nucleic Acids Res. 28 (21), 4317-4331 (2000)	gene CDS
JOURNAL MEDLINE PUBMED	Authors Takami, H. and Takaki, Y. Title Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 Natsushima, Yokosuka, Kanagawa 237-0061, Japan URL: http://www.jaustec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html , Tel: 81-468-67-3895, Fax: 81-468-66-6364	gene CDS
FEATURES source	1. 294250 Location/Qualifiers 1. "organism="Bacillus halodurans C-125" /mot_type="genomic DNA" /strain="C-125" /db_xref="taxon:27558"	gene CDS
gene	/note="alkaliphile" 236. .823 /gene="BH2879" 236. .823 /gene="BH2879"	gene CDS
gene	/codon_start=1 /transl_table=11 /product="spore cortex-lytic enzyme" /protein_id="BAB06588.1" /db_xref="GI:10175501" /translation="MMKFVLLFSCSILSFTLFTNKAESHSKHQVQSEDTLYLILSEQYVVMNLRDHDSPDNVTDVNGNVSQYIAECEPYAGKVAAGNGSLYFNPKATSPVSTRQQTIVGNHIFAK"	gene CDS
gene	/codon_start=1 /transl_table=11 /protein_id="BAB05603.1" /db_xref="GI:10175506" 1605	gene CDS

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/locus="B12.85"
/organism="zebrafish"
/feature="CDS"
/translation="MSNQEBERDFFTDLMGRPESTDVAENPQESTSGSTVEETKTE
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Query Match Score 40.4; DB 1; Length 294250;
Best Local Similarity 32.1%; Pred. No. 10;
Matches 50; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 23 AAAAATATTCCTCGAAAATATAATACATTGATTATTTATACAGTTATAA 82
Db 21297 AGAAATATAAAACAAAATATAAAATACAGTTATTCAGTTATAA 21298
Qy 83 TCAGAA 88
Db 21297 TCAGAA 21292

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```

RESULT 2
BX936455 BX936455 123707 bp DNA linear VRT 30-JUN-2004
LOCUS DEFINITION Zebrafish DNA sequence from clone DKEY-199112 in linkage group 20,
complete sequence.
ACCESSION BX936455
VERSION BX936455.9
KEYWORDS GI:495312650
SOURCE HTG
ORGANISM Danio rerio (zebrafish)
REFERENCE 1 (bases 1 to 123707)
AUTHORS Phillipmore, B.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone request: clonerquest@sanger.ac.uk
COMMENT On Jun 30, 2004 this sequence version replaced gi:4777603.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk

```

```

RESULT 3
BX957289 BX957289 152961 bp DNA linear HTG 07-JUN-2004
LOCUS DEFINITION Danio rerio clone CH211-232C6, 2 unordered pieces.
ACCESSION BX957289
VERSION BX957289.5
KEYWORDS GI:48426478
SOURCE HTGS PHASE1; HTGS CANCELLED.
ORGANISM Danio rerio
REFERENCE 1 (bases 1 to 152961)
AUTHORS Almeida, J.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridge, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone request: clonerquest@sanger.ac.uk
COMMENT On Jun 7, 2004 this sequence version replaced gi:46878815.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zc32C6
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 152/06 bases at least Q40
Consensus quality: 152/778 bases at least Q30
Consensus quality: 152/197 bases at least Q20
Insert size: 152/861; sum-of-contigs
Insert size: 158/260; 4.3% error; agarose-fp
Quality coverage: 7.35x in Q20 bases; sum-of-contigs Quality
coverage: 7.16x in Q20 bases; agarose-fp
-----
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only small overlaps as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the rare assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Mp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep_Clone-derived
-----
```

Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_reario/fishmask.shtml DKEY-199112

is from a Zebrafish BAC library

VECTOR: pIndigoBAC-5.

Location/Qualifiers

1. .123707

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/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="DKEY-199112"

/clone_lib="DanioKey"

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FEATURES source
ORIGIN

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Query Match Score 39.2; DB 5; Length 123707;
Best Local Similarity 38.3%; Pred. No. 22;
Matches 47; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 26 AAAATCTCGAAAATATTATAATACATTGATTTATACAGTATTATAA 85
Db 8300 AATATCATTTGAGATTTAACACAAATTGATTTAAATTATTAATGAA 8359

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```

RESULT 4
BX957289 BX957289 152961 bp DNA linear HTG 07-JUN-2004
LOCUS DEFINITION Danio rerio clone CH211-232C6, 2 unordered pieces.
ACCESSION BX957289
VERSION BX957289.5
KEYWORDS GI:48426478
SOURCE HTGS PHASE1; HTGS CANCELLED.
ORGANISM Danio rerio
REFERENCE 1 (bases 1 to 152961)
AUTHORS Almeida, J.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridge, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone request: clonerquest@sanger.ac.uk
COMMENT On Jun 7, 2004 this sequence version replaced gi:46878815.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zc32C6
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 152/06 bases at least Q40
Consensus quality: 152/778 bases at least Q30
Consensus quality: 152/197 bases at least Q20
Insert size: 152/861; sum-of-contigs
Insert size: 158/260; 4.3% error; agarose-fp
Quality coverage: 7.35x in Q20 bases; sum-of-contigs Quality
coverage: 7.16x in Q20 bases; agarose-fp
-----
```

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

Source 1. .4663 /organism="Drosophila sp." /mol_type="unassigned DNA" /db_xref="taxon:7242"

ORIGIN

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Qy 27 AAATCCCTCGAAATTAAATAATACATTGATTTTATACAGTTATAATGAG 86 Db 2341 AAATCCCTGAAAGCTTATATCCTACATAAAACTTGTGTTATAATGAGCTT 2282

Qy 87 AACTACATGAGCATAACGGCTAGGGGGAACTGAT 122 Db 2281 TACTACATGAGCCATCCATGATATCTTACATGAT 2246

RESULT 7 AC018035/c

LOCUS AC018035 41909 bp DNA Linear HTG 09-DEC-1999 DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.

ACCESSION AC018035

VERSION HTGS_PHASB2.

KEYWORDS

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster Arthropoda: Hexapoda: Insecta: Pterygota; Metazoa: Eukaryota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 41909)

AUTHORS Adams, M. and Venter, J.C.

TITLE Direct Submission

JOURNAL Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA

COMMENT This sequence was identified as CDM:10213107 by the submitter. For more information on this record e-mail to fly@celera.com.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced soon as it is available and the accession number will be preserved.

FEATURES

source 1. .41909 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227"

ORIGIN

Query Match 30.5%; Score 38.4; DB 2; Length 41909; Best Local Similarity 62.5%; Pred. No. 39; Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 27 AAATCCCTCGAAATTAAATAATACATTGATTTTATACAGTTATAATGAG 86 Db 21273 AAATCCCTGAAAGCTTATATCCTACATAAAACTTGTGTTATAATGAGCTT 21214

Qy 87 AACTACATGAGCATAACGGCTAGGGGGAACTGAT 122 Db 21213 TACTACATGAGCCATCTGATATCTTACATGAT 21178

RESULT 8 PFMAL7P1_13

WPCOMMENT Sequence split into 14 fragments LOCUS PFMAL7P1 Accession AL844506

Best Local Similarity Begin End

PFMAL7P1_00 1 100001 210000 PFMAL7P1_01 100001 310000 PFMAL7P1_02 200001 410000 PFMAL7P1_11 110001 121000 PFMAL7P1_12 120001 131000 PFMAL7P1_13 130001 1351552 Continuation (14 of 14) of PFMAL7P1 from base 13000001 (AL844506 Plasmodium falciparum 31)

Query Match 30.5%; Score 38.4; DB 2; Length 51552; Best Local Similarity 64.8%; Pred. No. 38; Matches 57; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 24 AAAAATCCTCGAAATTAAATAATACATTGATTTTATACAGTTATAATGAGCTT 83 Db 9554 AAAAAGATATAATATAGTACATAATAGTTTATATTATATATCAT 9613

Qy 84 GAGAACTACATGGCATACGGTGAGG 111 Db 9614 ATTATATTGATCCATACITGTGATG 9641

RESULT 9 PFMAL7P1_12

WPCOMMENT Sequence split into 14 fragments LOCUS PFMAL7P1 Accession AL844506

Best Local Similarity Begin End

PFMAL7P1_00 1 110000 PFMAL7P1_01 100001 210000 PFMAL7P1_02 200001 310000 PFMAL7P1_03 300001 410000 PFMAL7P1_04 400001 510000 PFMAL7P1_05 500001 610000 PFMAL7P1_06 600001 710000 PFMAL7P1_07 700001 810000 PFMAL7P1_08 800001 910000 PFMAL7P1_09 900001 1010000 PFMAL7P1_10 1000001 1110000 PFMAL7P1_11 1200001 1310000 PFMAL7P1_12 1300001 1351552 Continuation (13 of 14) of PFMAL7P1 from base 12000001 (AL844506 Plasmodium falciparum 31)

Query Match 30.5%; Score 38.4; DB 2; Length 110000; Best Local Similarity 64.8%; Pred. No. 34; Matches 57; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 24 AAAAATCCTCGAAATTAAATAATACATTGATTTTATACAGTTATAATGAGCTT 83 Db 109554 AAAAAGATATAATATAGTACATAATAGTTTATATTATATCAT 109613

Qy 84 GAGAACTACATGGCATACGGTGAGG 111 Db 109514 ATTATATTGATCCATACITGTGATG 109641

RESULT 10 AC007624/c

WPCOMMENT AC007624 167062 bp DNA linear HTG 13-DEC-1999

DEFINITION Drosophila melanogaster chromosome 2 clone BACR0F15 (D621) RPCL-98 10 F.15 map 42B-43A strain Y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.

ACCESSION AC007624

VERSION AC007624_5 GI:6563437

KEYWORDS HTG, HTGS_PHASE1.

SOURCE Drosophila melanogaster

ORGANISM Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Ephydriidae; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 167062)

AUTHORS Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,

one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source database: Em: EMBL; Sv: SWISSPROT; Tr: TREMBL; Mp: WORMPP; Information on the WORMPP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpp. This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl0>. RP1-108B14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>.

VECTOR: pEACe3.6
ORGANISM: "Homo sapiens"

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/evidence="not_experimental"

ORIGIN
Best Local Similarity 30.0%; Score 37.8; DB 9; Length 176577;

Matches 63; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 10 AGGGAGGGCAAGAAGAAATCTCGAAATATTATACATTGATTATTTA 69
Db 667672 AGAGTTGCCTAAAGTAAGTGCACAAATACTCTATCTGTATTATA 66703

Qy 70 TACGTATTATGAGACTAGTGGCATGGGAGGGGG 114
Db 667072 TAAGTTAGGACATTAAACTAACTAAGCTATCTGGTGGAGAG 66658

RESULT 14
AC095099 245135 bp DNA linear HTG 09-MAY-2003

DEFINITION Rattus norvegicus clone CH230-7118, WORKING DRAFT SEQUENCE, 2
unordered pieces.

ACCESSION AC095099
VERSION AC095099.6
KEYWORDS GT;30467746
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 245135)
AUTHORS Muzny, D. Marie., Metzger, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alstrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavarozzi, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, C., Durbin, K., Duval, B., Eaves, K., Egan, A., Escott, M., Eugene, C., Evans, C. A., Fallis, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisini, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Guevara, W., Guerra, W., Guevara, W., Hernandes, J., Hamilton, C., Hamilton, J., Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandes, J., Hernandez, R., Hines, S., Hlavak, S., Hume, J., Hume, J., Hollins, B., Howell, S., Hulyk, S., Hume, J., Jackson, A., Jackson, B., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karwathy, S., Kelly, S., Khan, Z., King, L., Kovari, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Loresuhewa, L., Louisegne, H., Lozada, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindarane, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meinen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundisba, M., Murphy, M., Nair, L., Nanckers, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakole, Ieme, O., Okonou, G., Olarpu, S., Olarpu, S., Parks, K., Pasternak, S., Paul, H., Perez, J. L., Pfannkoch, C., Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L., RL, Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodley, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sjösson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Suttorp, A., Svartek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wilezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yaku, S., Yen, J., Yoon, L., Yoon, L., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederauer, A., Weiss, R., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G., and Gibbs, R. A.

FEATURES
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/mol type="genomic DNA"
/db Xref="Raxxon:9608"
/Chromosome="10"
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/evidence="not_experimental"

JOURNAL
2 (bases 1 to 245135)
AUTHORS
TITLE
JOURNAL
Unpublished
Worley, K. C.
DIRECT SUBMISSION
DIRECT SUBMISSION
COMMENT
On May 9, 2003 this sequence version replaced gi:2494115.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.edu/project/str/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GCTX
Center clone name: CH230-7118

Summary Statistics
Assembly program: Atlas;
Consensus Quality: 229422 bases at least Q40
Consensus Quality: 232796 bases at least Q30

Consensus quality: 235239 bases at least Q20 Estimated insert size: 242725; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation					
* NOTE: Estimated insert size may differ from sequence length * (see http://www.hgsc.bcm.edu/docs/Cembank_draft_data.html) * NOTE: This is a 'working draft' sequence. It currently * consists of 2 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.					
* 1 242788: contig of 242788 bp in length * 242789 242888: gap of unknown length * 242889 245135: contig of 2247 bp in length.					
FEATURES	Location/Qualifiers				
	1. 1.245135				
	/organism="Rattus norvegicus"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:10116"				
	/clone="CH230-7118"				
	1. 1.1583				
	/note="wgs contig"				
	241315 .242788				
	/note="wgs contig"				
misc_feature					
misc_feature					
ORIGIN					
Query Match	29.8%	Score 37.6;	DB 2;	Length 245135;	
Best Local Matches	63.0%	Pred. No. 45;	DB 2;	Length 245135;	
Local Matches	58;	Conservative	0;	Gaps 0;	
Similarity		Mismatches 34;	Indels 0;	Gaps 0;	
/					
/	6	ACTTAGCCAGGCCAGAGAAAAATCTCGAAAAATTATACTATTGATTATT	65		
/	186244	ACTTTGAAATATAAAATCTCAATAGAGAAAAAGTAGACATTGAAATT	186		
/	66	TTTATACTAGTATTATAATGAGAACTACATGAG	97		
/	186304	TAGAAATTATCTCTATGTCATAATGTAAGAG	186335		
RESULT	15				
BX640454	165038 bp	DNA	linear	VRT 20-MAY-200	
LOCUS	6640454				

ACCESSION
NUMBER BX640454
VERSION 1.0
KEYWORDS HTG.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio (zebrafish)
COMMENT complete sequence.

1 (bases 1 to 165038)
AUTHORS Hammond, S.
TITLE Direct Submission
JOURNAL Submitted (20-May-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-heir@sanger.ac.uk. Clone requests: clone request@sanger.ac.uk
COMMENT On May 20, 2004 this sequence version replaced 91:46559191.
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit segments with

only a small overlap as described above. This sequence was finished as follows: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > = 30) compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: *EMBL*, *EMBL*; *Swi*, *SWISSPROT*; *Tr*, *TREMBL*; *Wp*, *WORMPP*; *Information*, *WormBase*; *Swi*, *SWISSPROT*; *Tr*, *TREMBL*; *Wp*, *WORMPP*; *Information*, *WormBase*. In the WORMPP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpp derived from the WORMPP database. The WORMPP database displays inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson et al., WashU). For further information see http://www.sanger.ac.uk/Projects/D_reario/fishmask.shtml CH211-1A19 (from CHORI-211 BAC library).

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson et al., WashU). For further information see http://www.sanger.ac.uk/Projects/D_reario/fishmask.shtml CH211-1A19 (from CHORI-211 BAC library).

Search completed: July 22, 2005, 07:46:27
Total time: 1893 SECs
Qy 81 AAT 83
Db 98757 TAT 98759

Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 22, 2005, 05:35:22 ; Search time 132 Seconds
(without alignments)
1561.901 Million cell updates/sec

Title: US-10-764-581-17
Perfect score: 126
Sequence: 1 catagactttagggggca.....tgaggggaaacatgtgaaac 126

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Parents_NA:*

1: /gn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /gn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /gn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /gn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /gn2_6/ptodata/1/ina/PCITS_COMA.seq:*

6: /gn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	36	28.6	91772	4	Sequence 15568, A
C 2	34.2	27.1	906	3	Sequence 4, App1
C 3	34.2	27.1	1619	1	Sequence 1, App1
C 4	34.2	27.1	1754	1	Sequence 2, App1
C 5	33.4	27.0	43333	4	Sequence 15381, A
C 6	33.6	26.7	20059	4	Sequence 3, App1
C 7	33.4	26.5	388559	4	Sequence 13384, A
C 8	33.4	26.5	388559	4	Sequence 13385, A
C 9	33.4	26.5	388559	4	Sequence 86, A
C 10	32.4	25.7	2625	3	Sequence 210, App1
C 11	32.2	25.6	1168	4	Sequence 4117, App1
C 12	32.2	25.6	1272	4	Sequence 60, App1
C 13	32.2	25.6	1309	6	Patent No. 5221624
C 14	32.2	25.6	1309	6	Patent No. 5221624
C 15	32.2	25.6	1536	4	Sequence 824, App1
C 16	32.2	25.6	1772	4	Sequence 542, App1
C 17	32.2	25.6	5848	3	Sequence 3, App1
C 18	32.2	25.6	7859	2	Sequence 4, App1
C 19	32.2	25.6	7859	2	Sequence 15, App1
C 20	32.2	25.6	7889	3	Sequence 15, App1
C 21	32.2	25.6	20598	4	Sequence 10, App1
C 22	32.2	25.6	53451	4	Sequence 15859, A
C 23	32.2	25.6	53451	4	Sequence 15859, A
C 24	32.2	25.6	9979	4	Sequence 15255, A
C 25	31.8	25.2	601	4	Sequence 79207, A
C 26	31.8	25.2	3387	1	Sequence 1, App1
C 27	31.8	25.2	450395	4	Sequence 15473, A

ALIGMENTS

RESULT 1
US-09-149-016-15568/c
; Sequence 15568, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FAST-SEQ For Windows Version 4.0
; SEQ ID NO 15568
; LENGTH: 91772
; TYPE: DNA

; ORGANISM: Human
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1)...(91772)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15568

Query Match 28.6% ; Score 36: DB 4; Length 91772;
Best Local Similarity 62.0%; Pred. No. 2.7;
Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 18 GCGAGAAAAAACTCTCGAAAATTATACTTATTTTACGATAT 77
Db 68218 CGAAAAAAAGACTAACAGACTAACAGACTAAATGTTATACTTACCCCTAT 68159

Qy 78 TATATACTGAACTAATGAGGGATACGGGTGA 109
Db 68158 TATTAACTGAAATTATACTGATACTGATAAA 68127

RESULT 2
US-09-149-016-15568/c
; Sequence 4, Application US/09586935
; Patent No. 6131267

; GENERAL INFORMATION:
; APPLICANT: KONG, HUIMIN
; APPLICANT: HIGGINS, LAUREN S.
; APPLICANT: DALTON, MICHAEL

APPLICANT: KUCERA, REBECCA B.
 ADDRESS: SCHILDKRAUT, IRA
 TITLE OF INVENTION: Cloning And Producing The N-BstNB1 Nicking Endonuclease

FILE REFERENCE: NEB-178
 CURRENT FILING DATE: 2000-06-02
 NUMBER OF SEQ ID NOS: 27
 SEQ ID NO: 4
 LENGTH: 906
 TYPE: DNA
 ORGANISM: *Bacillus stearothermophilus*
 FEATURE: CDS
 LOCATION: (1) .. (903)
 US-09-586-935-4

Query Match 27.1%; Score 34.2.; DB 3; Length 906;
 Best Local Similarity 58.3%; Pred. No. 3.4;
 Matches 60; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
 Qy 17 GCGAAGAAAAATCCTCGAAATTAAATACATGATTTATACAGTA 76
 Db 567 GCGAAACCAAAATGACTCTATGCTCTTGATCCATGATTTAGTGTATA 626

Qy 77 TTAAATGAGAACTACATGAGCCATGGTGAAGGGAACT 119
 Db 627 TCGAAATATGGAGTTACAGGTGATTCTGACCAAGGGACAT 669

RESULT 3
 US-08-507-455-1/c
 Sequence 1, Application US/08507455
 Patent No. 5695961
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: BIFUNCTIONAL EXPRESSION SYSTEM
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/507,455
 FILING DATE: 08-SEP-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9303988.1
 FILING DATE: 26-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: MITCHARD, LEONARD C
 REGISTRATION NUMBER: 29,009
 REFERENCE/DOCKET NUMBER: 1498-72
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1619 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Saccharomyces cerevisiae*
 FEATURE:

NAME/KEY: misc_recomb
 LOCATION: 546..547
 FEATURE:
 NAME/KEY: misc_recomb
 LOCATION: 635..636
 FEATURE:
 NAME/KEY: misc_recomb
 LOCATION: 1035..1036
 FEATURE:
 NAME/KEY: misc_recomb
 LOCATION: 1411..1412
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 550..555
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 574..579
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 668..673
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 692..697
 US-08-507-455-1

Query Match 27.1%; Score 34.2.; DB 1; Length 1619;
 Best Local Similarity 60.0%; Pred. No. 3.8;
 Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 Qy 1 CATAGACTTACGGGGCAAGAAAAATCTCGAAAATTATTAAATACATTGATT 60
 Db 1354 CATAGAAATATCGATGGAAAAAAACTGCATTAAGGCATTAATCATTAAG 1295
 Db 1294 TTTTTTTAATAAAATCTTAATAATCATTAAG 1260

RESULT 4
 US-08-507-455-1/c
 Sequence 2, Application US/08507455
 Patent No. 5695961
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: BIFUNCTIONAL EXPRESSION SYSTEM
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESS: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/507,455
 FILING DATE: 08-SEP-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9303988.1
 FILING DATE: 26-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: MITCHARD, LEONARD C
 REGISTRATION NUMBER: 29,009
 REFERENCE/DOCKET NUMBER: US/08/507,455
 FILING DATE: 08-SEP-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9303988.1
 FILING DATE: 26-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: MITCHARD, LEONARD C
 REGISTRATION NUMBER: 29,009
 REFERENCE/DOCKET NUMBER: 1498-72
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1754 base pairs
 TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic.c)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Saccharomyces cerevisiae*
 FEATURE:
 NAME/KEY: misc_recomb
 LOCATION: 546..547
 FEATURE:
 NAME/KEY: misc_recomb
 LOCATION: 635..636
 FEATURE:
 NAME/KEY: misc_recomb
 LOCATION: 1035..1036
 FEATURE:
 NAME/KEY: misc_recomb
 LOCATION: 1411..1412

US-08-507-455-2

Query Match 27.1%; Score 34.2; DB 1; Length 1754;
 Best Local Similarity 60.0%; Pred. Nc. 3..8;
 Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 CATAGACTTAGGGAGGCCAAGAAAAATCTCGAAAATTAAATACATTGATT 60
 Db 1486 CAYAGAAATTACATGGAAAAAAACTGATAAAGGGCATTAAGAGGGCATT 1427

Qy 61 TTATTTTATACAGTATATAATGAGAACTACATG 95
 Db 1426 TTTTTTTAATTTAAATCTTAATCTTAAAG 1392

RESULT 5
 US-09-949-016-15381
 Sequence 15381, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 15381
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-15381

Query Match 27.0%; Score 34; DB 4; Length 43333;
 Best Local Similarity 63.4%; Pred. Nc. 8;
 Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 18 GCAAGAAAAAATCTCGAAAATTAAATACATGATTATACAGT 77
 Db 17141 GCAAGACTCTGCTTAATTTAAATTTATTAATCT 17200

Qy 78 TATAATGAGAACTACATGAGGC 99
 Db 17201 TATAAAATTAATTTAGCC 17222

RESULT 6

US-09-734-674-3
 Sequence 3, Application US/09734674
 Patent No. 6438022
 GENERAL INFORMATION:
 APPLICANT: WEI, Ming-Hui et al.
 TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, NUCLEAR ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, AND USES THEREOF
 TITLE OF INVENTION:
 FILE REFERENCE: CL001018
 CURRENT APPLICATION NUMBER: US/09/734,674
 CURRENT FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 202001
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(202001)
 OTHER INFORMATION: n = A,T,C or G
 US-09-734-674-3

Query Match 26.7%; Score 33.6; DB 4; Length 202001;
 Best Local Similarity 61.4%; Pred. Nc. 14;
 Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 35 GAAATATTAAATATAATACATTGATTATTTACAGTATATAATGAGAACTCAT 94
 Db 191642 GAGAAATATTCAATACCTCTCATTTATTAATCAATAACAAAT 191701

Qy 95 GAGGCAATAGGGTGGGGAACTGAT 122
 Db 191702 GGGCATACACATACAATGGGACAT 191729

RESULT 7
 US-09-949-016-13384
 Sequence 13384, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 13384
 LENGTH: 38559
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(38559)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-13384

Query Match 26.5%; Score 33.4; DB 4; Length 38559;
 Best Local Similarity 60.4%; Pred. Nc. 11;
 Matches 55; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 2 ATAGACTTAGGGAGGGCTGTTGAAATGAGCAAGCTTACTACTT 61
 Db 37868 ATATGCGGGTGTGAAATGAGCAAGCTTACTACTT 37927

OTHER INFORMATION: n = A, T, C or G
US-09-949-016-13386

Query Match 26.5%; Score 33.4; DB 4; Length 38559;
Best Local Similarity 60.4%; Pred. No. 11;
Matches 55; Mismatches 0; N mismatches 36; Indels 0; Gaps 0;

Qy 2 ATAGACTTAGGGAGGGCAAGAAAAATCCTCGAAATTATACATTGATT 61
Db 37868 ATAATCTGGGTGTGAAATAGAAACATCGCAAGCATATTTTACTATT 37927

Query Match 26.5%; Score 33.4; DB 4; Length 38559;
Best Local Similarity 60.4%; Pred. No. 11;
Matches 55; Mismatches 0; N mismatches 36; Indels 0; Gaps 0;

Qy 2 ATAGACTTAGGGAGGGCAAGAAAAATCCTCGAAATTATACATTGATT 61
Db 37868 ATAATCTGGGTGTGAAATAGAAACATCGCAAGCATATTTTACTATT 37927

RESULT 10
US-09-453-702B-210/C
; Sequence 210, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 13385
; LENGTH: 38559
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (38559)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-13385

Query Match 26.5%; Score 33.4; DB 4; Length 38559;
Best Local Similarity 60.4%; Pred. No. 11;
Matches 55; Mismatches 0; Gaps 0;

Qy 2 ATAGACTTAGGGAGGGCAAGAAAAATCCTCGAAATTATACATTGATT 61
Db 37868 ATAATCTGGGTGTGAAATAGAAACATCGCAAGCATATTTTACTATT 37927

Query Match 26.5%; Score 33.4; DB 4; Length 38559;
Best Local Similarity 60.4%; Pred. No. 11;
Matches 55; Mismatches 0; Gaps 0;

Qy 2 ATAGACTTAGGGAGGGCAAGAAAAATCCTCGAAATTATACATTGATT 61
Db 37868 ATAATCTGGGTGTGAAATAGAAACATCGCAAGCATATTTTACTATT 37927

RESULT 9
US-09-949-016-13386
; Sequence 13386, Application US/0949016
; Patent No. 631339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 13386
; LENGTH: 38559
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (38559)

Query Match 25.7%; Score 32.4; DB 3; Length 2625;
Best Local Similarity 56.6%; Pred. No. 13;
Matches 60; Mismatches 0; N mismatches 46; Indels 0; Gaps 0;

Qy 18 GCAAGGAAAAATCCTCGAAATTATACATTGATTATTTATACAGTAT 77
Db 2419 GTAAAPAGACAATACCTCTATAATGCGAAATTGTGATTTAAATGAA 2360

Query Match 25.7%; Score 32.4; DB 3; Length 2625;
Best Local Similarity 56.6%; Pred. No. 13;
Matches 60; Mismatches 0; N mismatches 46; Indels 0; Gaps 0;

Qy 18 GCAAGGAAAAATCCTCGAAATTATACATTGATTATTTATACAGTAT 77
Db 2419 GTAAAPAGACAATACCTCTATAATGCGAAATTGTGATTTAAATGAA 2360

RESULT 11

Db 2359 CCTTATTAATCTACAACCTTCATATGGGGAAAGAAATG 2314

Qy 99 CATACTGGTGGGGGA 115
Db 1108 CTTCATGTGAGGTA 1092

RESULT 13

5221624-4/c

; Patent No. 5221624
; APPLICANT: BLAIR, LINDLEY C.; KODURI, JAR-HOW; WEICKMANN, JOACHIM J.
; TITLE OF INVENTION: DNA ENCODING (LYS46, ASP97, ASP113) AND (LYS16, ASP113, ASP137) THAMATIN I
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/407,416
; FILING DATE: 14-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 268,702
; FILING DATE: 08-NOV-1988
; SEQ ID NO: 4:
; LENGTH: 1309

5221624-4

Query Match 25.6%; Score 32.2; DB 6; Length 1309;
Best Local Similarity 61.2%; Pred. No. 13;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CATACTGGTGGGGCAGAAAAATCCTCGAAATTATTAAATATACATGATT 60
Db 1242 CTAGAAATATCGATGGAAAAAACCTGATAAAGGCATTAAAGGGACGAAAT 1183

RESULT 14

5221624-4/c

; Patent No. 5221624
; APPLICANT: BLAIR, LINDLEY C.; KODURI, JAR-HOW; WEICKMANN, JOACHIM J.
; TITLE OF INVENTION: DNA ENCODING (LYS46, ASP97, ASP113) AND (LYS16, ASP113, ASP137) THAMATIN I
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/407,416
; FILING DATE: 14-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 268,702
; FILING DATE: 08-NOV-1988
; SEQ ID NO: 4:
; LENGTH: 1309

5221624-4

Query Match 25.6%; Score 32.2; DB 6; Length 1309;
Best Local Similarity 61.2%; Pred. No. 13;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CATACTGGTGGGGCAGAAAAATCCTCGAAATTATTAAATATACATGATT 60
Db 1242 CTAGAAATATCGATGGAAAAAACCTGATAAAGGCATTAAAGGGACGAAAT 1183

RESULT 15

US-09-655-824/c

; Sequence 824, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: COCKS, BENJAMIN G.

Qy 39 ATTATTAAATACATTTGATTATTATACAGTATAATGAGAACTACATGAGG 98
Db 1168 ATTATTAGTATAATTTGCTTGTGTTTATACAGATATAAGATTCCCTCATAT 1109

APPLICANT: Susan G. Stuart
 ATTORNEY: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 NUMBER OF SEQUENCES: 1508
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655
 FILING DATE: HEREWITH
 CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 824:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1536 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: BRAUT03
 CLONE: 859619

US-09-023-655-024

Query Match 25.6%; Score 32.2; DB 4; Length 1536;
 Best Local Similarity 63.6%; Pred. No. 13;
 Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 39 ATTATTAATAATACATTGATTATTATAAGTATAATAGAACTACATGAGG 98
 Db 1277 ATTTAGTATAATTTGCTTGTGTTTACAGATAAATAGTTCTCATTAAT 1218

Qy 99 CATAACGGGTGAGGGGA 115
 Db 1217 CTTCGGATGAGGGTA 1201

Search completed: July 22, 2005, 08:41:12
 Job time : 137 secs

Result No.	Score	Query	Match	Length	DB ID	Description
SUMMARIES						
1	126	100.0	126	21	US-10-764-581-17	Sequence 17, Appl
c 2	36.4	28.9	2121	17	US-10-764-581-17	Sequence 3339, Ap
c 3	36	28.6	6112	9	US-10-398-221-3339	Sequence 2662, Ap
c 4	36	28.6	6112	9	US-09-164-877-2662	Sequence 2663, Ap
c 5	36	28.6	6112	17	US-10-242-515-2662	Sequence 2662, Ap
c 6	36	28.6	6112	17	US-10-242-515-2662	Sequence 2663, Ap
c 7	35.6	28.3	2084	20	US-10-425-115-16651	Sequence 16651,
c 8	35.6	28.3	5237	19	US-10-433-793-138	Sequence 138, Appl
c 9	35.4	28.1	27587	11	US-09-997-722-253	Sequence 253, Appl
c 10	35.2	27.9	367378	16	US-10-312-841-2	Sequence 2, Appl
c 11	35	27.8	585	13	US-10-057-632-221-497	Sequence 221497,
c 12	35	27.8	585	17	US-10-057-632-221-497	Sequence 221497,
c 13	34.8	27.6	49569	17	US-10-398-221-8	Sequence 8, Appl
c 14	34.8	27.6	301208	17	US-10-398-221-8	Sequence 8, Appl
c 15	34.4	27.3	7450	15	US-10-240-453-5	Sequence 5, Appl
c 16	34.4	27.3	237981	18	US-10-433-580-2	Sequence 2, Appl
c 17	34.2	27.1	906	17	US-10-276-289-4	Sequence 4, Appl
c 18	34.2	27.1	5391	15	US-10-311-455-215	Sequence 215, Appl
c 19	34.2	27.1	5391	15	US-10-311-455-215	Sequence 215, Appl
c 20	34.2	27.1	8166	15	US-10-311-455-1765	Sequence 1765, Appl
c 21	33.8	26.8	5489	15	US-10-311-455-2094	Sequence 2094, Appl
c 22	33.8	26.8	15853	17	US-10-221-613-421	Sequence 421, Appl
c 23	33.6	26.7	138887	19	US-10-322-281-146	Sequence 146, Appl
c 24	33.6	26.7	202001	9	US-09-734-674-3	Sequence 3, Appl
c 25	33.6	26.7	202001	14	US-10-311-455-990-3	Sequence 3, Appl
c 26	33.6	26.7	202001	24	US-11-061-822-3	Sequence 3, Appl
c 27	33.4	26.5	15313	15	US-10-311-455-440	Sequence 440, Appl
c 28	33.2	26.3	2000	9	US-09-938-842A-4553	Sequence 4553, Appl
c 29	33.2	26.3	2000	11	US-09-938-842A-4553	Sequence 4553, Appl
c 30	33.2	26.3	14887	15	US-10-311-455-604	Sequence 604, Appl
c 31	33.2	26.3	380963	22	US-11-274-990-3	Sequence 5, Appl
c 32	33.2	26.3	380963	22	US-10-765-790-5	Sequence 5, Appl
c 33	33	26.2	201	20	US-10-719-991-20393	Sequence 20393, Pub
c 34	33	26.2	201	20	US-10-719-993-50769	Sequence 50769, Pub
c 35	33	26.2	201	21	US-10-741-600-40227	Sequence 40227, Pub
c 36	33	26.2	201	21	US-10-741-600-67698	Sequence 67698, Pub
c 37	33	26.2	777	13	US-10-057-632-32741	Sequence 32741, Pub
c 38	33	26.2	777	17	US-10-057-632-32741	Sequence 32741, Pub
c 39	33	26.2	13784	17	Sequence 144, Appl	
c 40	33	26.2	201	20	Sequence 7017, Appl	
c 41	33	26.2	24338	21	Sequence 17939, Appl	
c 42	33	26.2	1980090	20	Sequence 6815, Appl	
c 43	33	26.2	26308	21	Sequence 17676, Appl	
c 44	32.8	26.0	6308	15	Sequence 1444, Appl	
c 45	32.8	26.0	17869	15	Sequence 77, Appl	

Qy 61 TTATTTTATACAGTATTATAATGAGAAGTACATGAGGCAATACGGCATACGGGTGAGGGAAACATG 120
 Db 61 TTATTTTATACAGTATTATAATGAGAAGTACATGAGGCAATACGGCATACGGGTGAGGGAAACATG 120

Qy 121 ATGAAAC 126
 Db 121 ATGAAAC 126

RESULT 2

US-10-398-221-3339/c
 Sequence 3339, Application US/10398221
 Publication No. US20040018514A1
 GENERAL INFORMATION:
 APPLICANT: KUNST, Frederik
 ATTORNEY: GLASER, Philippe
 TITLE OF INVENTION: Listeria innocua, genome and applications
 FILE REFERENCE: 344 702 - US
 CURRENT APPLICATION NUMBER: US/10/398.221
 CURRENT FILING DATE: 2003-03-27
 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 PRIOR FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: FR 00/12 697
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 4025
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3339
 LENGTH: 2121
 TYPE: DNA
 ORGANISM: Listeria monocytogenes 4b
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1): 'end'
 OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u

US-10-398-221-3339

Query Match 28.9%; Score 36.4%; DB 17; Length 2121;
 - Matches 61; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
 - Matches 61; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 24 AAAAATCTCGAAAATTATAATACATGTTTACAGTTATAAT 83
 Db 219 AAAATGTTAAATATAATACATGTTACATATAATCATCTATAAT 160

Qy 84 GAGAACYCATGGCATACGGGTGAGGGGACATGAA 125
 Db 159 GAAAGTATCATTAAATTAACGGGGGTAGGTGAA 118

RESULT 3

US-09-764-877-2662/c
 Sequence 2662, Application US/09764877
 Publication No. US20047140A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et. al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PC005
 CURRENT APPLICATION NUMBER: US/09/764,877
 CURRENT FILING DATE: 2001-01-17
 PRIOR APPLICATION data removed - refer to PALM or file wrapper
 NUMBER OF SEQ ID NOS: 4031
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2662
 LENGTH: 6112
 TYPE: DNA
 ORGANISM: Homo sapiens

RESULT 4

US-09-764-877-2663/c
 Sequence 2663, Application US/09764877
 Patent No. US20020147140A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et. al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PC005
 CURRENT APPLICATION NUMBER: US/09/764,877
 CURRENT FILING DATE: 2001-01-17
 PRIOR application data removed - refer to PALM or file wrapper
 NUMBER OF SEQ ID NOS: 4031
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2663
 LENGTH: 6112
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-764-877-2663
 Query Match 28.6%; Score 36; DB 9; Length 6112;
 Best Local Similarity 62.0%; Pred. No. 1.1e+02;
 Matches 57; Mismatches 35; Indels 0; Gaps 0;
 Qy 18 GCAAGAAAAAAATCTCTCGAAAATTATAATACATGTTTACAGTTATACTAGT 77
 Db 2667 GGAAAGAAAAAGGTAACTAACAGGTTAAATGGGATAATGTACCTAT 2608

Qy 78 TATAATGAGAAGTACATGGCATACGGGTGAA 109
 Db 2607 TATTAAAGGTTATAATGAACTGATA 2576

RESULT 5

US-10-242-515-2662/c
 Sequence 2662, Application US/10242515
 Publication No. US2004000948A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et. al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PC005CL
 CURRENT APPLICATION NUMBER: US/10/242,515
 CURRENT FILING DATE: 2002-09-13
 PRIOR APPLICATION NUMBER: 09/764,877
 PRIOR FILING DATE: 2001-01-17
 PRIOR APPLICATION NUMBER: 60/179,065
 PRIOR FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: 60/180,628
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: 60/214,886
 PRIOR FILING DATE: 2000-06-28
 PRIOR APPLICATION NUMBER: 60/217,487
 PRIOR FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/225,758
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/220,963
 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: 60/217,496
 PRIOR FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/225,447
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/218,290
 PRIOR FILING DATE: 2000-07-14
 Remaining Prior Application data removed - See File wrapper or PALM.
 NUMBER OF SEQ ID NOS: 4031
 SOFTWARE: PatentIn Ver. 2.0

Qy 18 GCAAGAAAAAAATCTCTCGAAAATTATAATACATGTTTACAGTTAT 77

/ TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 / FILE REFERENCE: A-71171/RMS/DCF
 / CURRENT APPLICATION NUMBER: US/09/997,722
 / CURRENT FILING DATE: 2001-11-30
 / PRIORITY NUMBER: US 09/747,377
 / PRIORITY FILING DATE: 2000-12-22
 / PRIORITY APPLICATION NUMBER: US 09/798,586
 / PRIORITY FILING DATE: 2001-03-02
 / NUMBER OF SEQ ID NOS: 301
 / SOFTWARE: Patentin version 3.1
 / SEQ ID NO: 253
 / LENGTH: 27587
 / TYPE: DNA
 / ORGANISM: Mus musculus
 / US-09-997-722-253

Query Match 28.1%; Score 35.4%; DB 11; Length 27587;
 Best Local Similarity 63.5%; Pred. No. 2.3e-02;
 Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 3 3 TCGAAATTATAATACATTGATTATTATACAGTATTATAATGAGACTAC 92
 Db 7439 TCAAACATATATATATATATTTTTTTCTTCTACTAGCTGGAACTG 7498

Query Match 28.1%; Score 35.4%; DB 11; Length 27587;
 Best Local Similarity 63.5%; Pred. No. 2.3e-02;
 Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 93 ATGAGGCTACGGTAGGGAAC 117
 Db 7499 CCAAGGGATTCATGTGGAAATC 7523

RESULT 10
 US-10-312-841-2

/ Sequence 2, Application US/10312841
 / Publication No. US20030186277A1

/ GENERAL INFORMATION:
 / APPLICANT: Epigenomics AG
 / TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
 / FILE REFERENCE: E01/1208/WO

/ CURRENT APPLICATION NUMBER: US/10/312,841
 / CURRENT FILING DATE: 2002-12-30
 / NUMBER OF SEQ ID NOS: 2
 / SEQ ID NO: 2
 / LENGTH: 3673778

/ OTHER INFORMATION:
 / FEATURE: chemically treated genomic DNA (Homo sapiens)
 / NAME/KEY: unsure
 / LOCATION: (379615)
 / US-10-312-841-2

Query Match 27.9%; Score 35.2%; DB 16; Length 3673778;
 Best Local Similarity 60.4%; Pred. No. 7e+02;
 Matches 58; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 3 TAGACTTAGGGAGGGCAAGAAGAAATCTCGAAATATAATACATTGATT 62
 Db 1030773 TAGTTTAGGGAGGATAGGGAGTATAGAGATTGTTAATTTGATATT 1030832

Query Match 27.8%; Score 35%; DB 17; Length 585;
 Best Local Similarity 64.9%; Pred. No. 1.1e-02;
 Matches 50; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

Qy 63 ATTTTATACAGTATTATAATGAGAATCATGAGG 98
 Db 1030833 TTTTTTTGTGTGTATTAATTTATGAGG 1030868

RESULT 11
 US-10-027-632-221497/c

/ Sequence 221497, Application US/10027632
 / Publication No. US20020198371A1

/ GENERAL INFORMATION:
 / APPLICANT: Wang, David G.
 / TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 / FILE REFERENCE: 108827.129

/ CURRENT APPLICATION NUMBER: US/10/027,632
 / CURRENT FILING DATE: 2002-04-10
 / PRIORITY NUMBER: US 60/218,006
 / PRIORITY FILING DATE: 2000-07-12
 / PRIORITY APPLICATION NUMBER: US 60/198,676
 / PRIORITY FILING DATE: 2000-04-20
 / PRIORITY APPLICATION NUMBER: US 60/193,483
 / PRIORITY FILING DATE: 2000-05-29
 / PRIORITY APPLICATION NUMBER: US 60/185,218
 / PRIORITY FILING DATE: 2000-02-24
 / PRIORITY APPLICATION NUMBER: US 60/167,363
 / PRIORITY FILING DATE: 1999-11-23
 / PRIORITY APPLICATION NUMBER: US 60/156,358
 / PRIORITY FILING DATE: 1999-09-28
 / PRIORITY APPLICATION NUMBER: US 60/146,002
 / PRIORITY FILING DATE: 1999-08-09
 / PRIORITY APPLICATION NUMBER: US 60/146,002
 / PRIORITY FILING DATE: 2000-02-24
 / PRIORITY APPLICATION NUMBER: US 60/167,363
 / PRIORITY FILING DATE: 1999-11-23
 / PRIORITY APPLICATION NUMBER: US 60/156,358
 / PRIORITY FILING DATE: 1999-09-28
 / PRIORITY APPLICATION NUMBER: US 60/146,002
 / NUMBER OF SEQ ID NOS: 325720
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 221497
 / LENGTH: 585
 / TYPE: DNA
 / ORGANISM: Human
 / US-10-027-632-221497

Qy 14 AGGGCAAGAAAAATCCTCGAAAATTATTAAATACATTGATTATTATATACA 73
 Db 242 AGGAAAGTAAAGATCAAATACAGTAAATTGATGAAATTATTCT 183

Qy 74 GATTATATGAGACT 90
 Db 182 ATATTCCCTGACAGCT 166

RESULT 13
 US-10-398-221-8
 ; Sequence 8, Application US/10398221
 ; Publication No. US20040018514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNST, Frederik
 ; ATTORNEY: GLASER, Philippe
 ; TITLE OF INVENTION: Listeria innocua, genome and applications
 ; FILE REFERENCE: 344 702 - US
 ; CURRENT APPLICATION NUMBER: US/10/398,221
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 ; PRIOR FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: FR 00/12 697
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 4025
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 8
 ; LENGTH: 495269
 ; TYPE: DNA
 ; ORGANISM: Listeria innocua
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(end)
 ; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
 us-10-398-221-8

Query Match 27.6%; Score 34.8%; DB 17; Length 495269;
 Best Local Similarity 58.8%; Pred. No. 6.5e+02; Indels 0; Gaps 0;
 Matches 60; Conservative 0; Mismatches 42;

Qy 24 AAAAATCCTCGAAAATTATTAAATACATTGATTATTATACATTATAAT 83
 Db 115445 AAAATCTTAAATTAATTAATTAATTAATTAATCATCTATAT 115504

Qy 84 GAGACTACATGAGCATACGGTGAAGGGACATGATGAA 125
 Db 115505 GAAAGTATCATTAAATTAACGGGAGGGTTAGGTGAA 115546

RESULT 14
 US-10-398-221-2055/c
 ; Sequence 2058, Application US/10398221
 ; Publication No. US20040018514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNST, Frederik
 ; ATTORNEY: GLASER, Philippe
 ; TITLE OF INVENTION: Listeria innocua, genome and applications
 ; FILE REFERENCE: 344 702 - US
 ; CURRENT APPLICATION NUMBER: US/10/398,221
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 ; PRIOR FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: FR 00/12 697
 ; NUMBER OF SEQ ID NOS: 4025
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 2058
 ; LENGTH: 3011208
 ; TYPE: DNA
 ; ORGANISM: Listeria innocua
 us-10-398-221-2058

Query Match 27.6%; Score 34.8%; DB 17; Length 3011208;
 Best Local Similarity 58.8%; Pred. No. 8.3e+02; Indels 0; Gaps 0;
 Matches 60; Conservative 0; Mismatches 42;

Qy 24 AAAAATCCTCGAAAATTATTAAATACATTGATTATTATACATTATAAT 83
 Db 1643510 AAAATAGTTAAATTAATTAATTAATTAACATTACATCTATAAT 1643451

Qy 84 GAGACTACATGAGCATACGGTGAAGGGACATGATGAA 125
 Db 1643450 GAAAGTATCATTAAATTAACGGGAGGGTTAGGTGAA 1643409

RESULT 15
 US-10-240-453-5/c
 ; Sequence 5, Application US/10240453
 ; Publication No. US20030148326A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OLEK, Alexander
 ; ATTORNEY: PIEPENBROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
 ; TITLE OF INVENTION: Transcription
 ; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
 ; TITLE OF INVENTION: With DNA Transcription
 ; FILE REFERENCE: 5013-1009
 ; CURRENT APPLICATION NUMBER: US/10/240,453
 ; CURRENT FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03973
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019059.8
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: DE 10032529.7
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: DE 10043826.1
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 350
 ; SEQ ID NO: 5
 ; LENGTH: 7450
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (4653, 5152, 5156..5157, 5722)
 us-10-240-453-5

Query Match 27.3%; Score 34.4%; DB 15; Length 7450;
 Best Local Similarity 65.8%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
 Matches 50; Conservative 0; Mismatches 26;

Qy 19 CAAGAAAAAATCCGAAATTATAATACATTGATTATTATACATT 78
 Db 567 CCACAAAAATCCCTCAAAATCTATTTATTTAAATTAATTAAT 508

Qy 79 ATAATGAGAACTACAT 94
 Db 507 AAACAAATATATAT 492

Search completed: July 22, 2005, 10:24:46
 Job time : 625 secs

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries									
Database :	EST:*								
	1: gb_est1:*								
	2: gb_est2:*								
	3: gb_hcc:*								
	4: gb_es3:*								
	5: gb_es4:*								
	6: gb_es5:*								
	7: gb_es6:*								
	8: gb_g881:*								
	9: gb_g882:*								
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.								
SUMMARIES									
Result No.	Score	Query Match	Length	DB	ID	Description			
1	38.8	30.8	266	4	BM274717	BM274717 PESToaa7			
C 2	38.8	30.8	462	5	BP735538	BP735538			
C 3	38.8	30.8	479	4	BP720714	BP720714			
C 4	38.8	30.8	497	4	Bu629764	Bu629764			
C 5	38	30.2	1101	9	CNS017JM	AL108124 Drosophil			
C 6	38	30.2	1134	9	CL103280	CL103280			
C 7	37.2	29.2	792	7	CF284280	CF284280			
C 8	37	29.4	312	5	BP721218	BP721218			
C 9	37	29.4	542	4	BG143667	BG143667			
C 10	36.8	29.4	635	9	CE073145	CE073145			
C 11	36.8	29.2	309	1	AV207641	AV207641			
C 12	36.8	29.2	319	1	AV101294	AV101294			
C 13	36.8	29.2	451	5	Bu070396	Bu070396			
C 14	36.8	29.2	457	4	BM310085	BM310085			
C 15	36.8	29.2	459	4	H49659	H49659			
C 16	36.8	29.2	474	4	BH310349	BH310349			
C 17	36.8	29.2	534	5	BQ787408	BQ787408			
C 18	36.8	29.2	659	1	AL652174	AL652174			
C 19	36.8	29.2	689	8	BZ322030	BZ322030			
C 20	36.8	29.2	708	1	AL646926	AL646926			
C 21	36.8	29.2	746	5	BX749863	BX749863			
C 22	36.8	29.2	1011	9	CNS014Z0	AL104614 Drosophil			
C 23	36.4	28.9	228	4	BH338343	BH338343			
C 24	36.4	28.9	612	8	BH645122	BH645122			

priming, size-selected and directionally cloned into the EcoRI (5' end) to XbaI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the Expressist helper phage (Stratagene). Clones were mass excised using the Expressist helper phage (Stratagene), the phagemids were precipitated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells. Clone Availability: David Sibley, Washington University. "

ORIGIN
 Query Match 30.8%; Score 38.8; DB 4; Length 266;
 Best Local Similarity 67.1%; Pred. No. 62;
 Matches 55; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 Qy 20 AGAGAAAAACTCTCGAAATTAAATACATTGATTATACAGTTA 79
 Db 129 AAAAAGAAAAAAATAGTAAATTAAATATATATATATATATATAAA 188
 Qy 80 TAATGAACTACATGAGGCAT 101
 Db 189 TAATGTTAACATATGAGGACAT 210

RESULT 2
 LOCUS BP735538/c 462 bp mRNA linear EST 19-JUL-2004
 DEFINITION BP735538 Osada Taira anterior neuroectoderm (ANE) pCS105 cDNA
 LIBRARY Xenopus laevis cDNA clone XL505k03ex 3', mRNA sequence.
 ACCESSION BP735538
 VERSION BP735538.1 GI:46084131
 EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopoda; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 REFERENCE Osada, S., Kitayama, A., Ueno, N. and Taira, M.
 AUTHORS Osada, S., Kitayama, A., Ueno, N. and Taira, M.
 TITLE Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos
 Unpublished (2004)
 JOURNAL Contact: Masanori Taira
 Department of Biological Sciences, University of Tokyo; CREST, Japan
 Science and Technology Corporation, Japan
 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
 Tel: 81-03-5841-4434
 Fax: 81-03-5841-4434
 Email: m_taira@bio1.s.u-tokyo.ac.jp
 URL: http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.

FEATURES Source
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="XL447b21ex"
 /tissue_type="anterior neuroectoderm"
 /dev_stage="late gastrula (stage 12.5)"
 /clone_lib="Osada Taira anterior neuroectoderm (ANE)"
 /Location/Qualifiers
 1..479
 ORIGIN
 Query Match 30.8%; Score 38.8; DB 5; Length 479;
 Best Local Similarity 60.4%; Pred. No. 59;
 Matches 64; Conservative 0; Mismatches 42; Indels 0;
 Gaps 0;
 Qy 7 CTTAGGAGGGCAGAAAAATCTCGAAAATATTATATACATTGATTATT 66
 Db 250 CTTAGTGTGATCAGTACAGCTACTGTAAATTACAGGAAAATCATTT 191
 Qy 67 TTATACAGTATTATAATGAGAAGTACATGAGGATACAGGGTGAAGG 112
 Db 190 TTAAATATTGATTATGATCATATGGAGTCTATGGAGACGG 145

RESULT 4
 LOCUS BJ629764/c 497 bp mRNA linear EST 01-OCT-2003
 DEFINITION Xenopus laevis normalized Xenopus early gastrula library
 LIBRARY Xenopoda; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 REFERENCE 1 (bases 1 to 497)
 AUTHORS Kohara, Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)

Db 168 TTAAATATTGATTATGATCATATGGAGTCTATGGAGACGG 123
 RESULT 3
 LOCUS BP720714/c 479 bp mRNA linear EST 19-JUL-2004
 DEFINITION BP720714 Osada Taira anterior neuroectoderm (ANE) pCS105 cDNA
 LIBRARY Xenopus laevis cDNA clone XL447b21ex 3', mRNA sequence.
 ACCESSION BP720714
 VERSION BP720714.1 GI:46069307
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Xenopus.
 REFERENCE 1 (bases 1 to 479)
 AUTHORS Osada, S., Kitayama, A., Ueno, N. and Taira, M.
 TITLE Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos
 Unpublished (2004)
 JOURNAL Contact: Masanori Taira
 Department of Biological Sciences, University of Tokyo; CREST, Japan
 Science and Technology Corporation, Japan
 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
 Tel: 81-03-5841-4434
 Fax: 81-03-5841-4434
 Email: m_taira@bio1.s.u-tokyo.ac.jp
 URL: http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.

FEATURES Source

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="XL447b21ex"

/tissue_type="anterior neuroectoderm"

/dev_stage="late gastrula (stage 12.5)"

/clone_lib="Osada Taira anterior neuroectoderm (ANE)"

/Location/Qualifiers

1..479

ORIGIN

Query Match 30.8%; Score 38.8; DB 5; Length 479;

Best Local Similarity 60.4%; Pred. No. 59;

Matches 64; Conservative 0; Mismatches 42; Indels 0;

Gaps 0;

Qy 7 CTTAGGAGGGCAGAAAAATCTCGAAAATATTATACATTGATTATT 66

Db 250 CTTAGTGTGATCAGTACAGCTACTGTAAATTACAGGAAAATCATTT 191

Qy 67 TTATACAGTATTATAATGAGAAGTACATGAGGATACAGGGTGAAGG 112

Db 190 TTAAATATTGATTATGATCATATGGAGTCTATGGAGACGG 145

RESULT 4

LOCUS BJ629764

DEFINITION Xenopus laevis normalized Xenopus early gastrula library

LIBRARY Xenopoda; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 497)

AUTHORS Kohara, Y.

TITLE Expressed genes in X. laevis embryo

JOURNAL Unpublished (2001)

ORGANISM

Xenopus laevis

(African clawed frog)

COMMENT

Unpublished (2004)

JOURNAL Contact: Masanori Taira

Department of Biological Sciences, University of Tokyo; CREST, Japan

Science and Technology Corporation, Japan

7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

Tel: 81-03-5841-4434

Fax: 81-03-5841-4434

Email: m_taira@bio1.s.u-tokyo.ac.jp

URL: http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.

FEATURES Source

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="XL505k03ex"

/tissue_type="anterior neuroectoderm"

/dev_stage="late gastrula (stage 12.5)"

/clone_lib="Osada Taira anterior neuroectoderm (ANE)"

/Location/Qualifiers

1..462

ORIGIN

Query Match 30.8%; Score 38.8; DB 5; Length 462;

Best Local Similarity 60.4%; Pred. No. 59;

Matches 64; Conservative 42; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CTTAGGAGGGCAGAAAAATCTCGAAAATATTATACATTGATTATT 66

Db 228 CTTAGTGTGATCAGTACAGCTACTGTAAATTACAGGAAAATCATTT 169

Qy 67 TTATACAGTATTATAATGAGAAGTACATGAGGATACAGGGTGAAGG 112

COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856
Fax: 81-559-81-5555
Email: taininogenes.nig.ac.jp

The information of this clone is available through the following URL.
<http://xenopus.nibb.ac.jp/>

FEATURES source
1. Location/Qualifiers
1..497
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="TAXON:8355"
/clone="XLI62K22"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus·early gastrula library"

ORIGIN

Query Match 30.8%; Score 38.4; DB 4; Length 497;
Best Local Similarity 60.4%; Pred. No. 59;
Matches 64; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 7 CTTAGGGGGCGAAGAAAAAAATCCCTCGAAATTATAATATGATTGATTATT 66
Db 274 CTTAGCTGGATCAAGTACAAGTCTACTGTTAATTATACAGAAAAATTGAAATCATTT 215

Qy 67 TTTACAGCTTATAATGAGAACTACATGAGGCTACGGGTAGGG 112
Db 214 TTTAAATTTGGATTATTGATCATATGGAGCTCATGGAGACGG 169

RESULT 5 CNS017JM/c LOCUS DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC 1101 bp DNA linear GSS 26-JUL-1999

Drosophila melanogaster genome survey sequence SP6 end of BAC 1101 bp DNA linear GSS 26-JUL-1999

ACCESSION AL108124
KEYWORDS SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Drosophidae; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope

TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cnrs.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk/> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Geneviève Payan. It has been constructed in the vector pBeloBAC1.

FEATURES source
1. Location/Qualifiers
1..1101
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/mol_type="genomic DNA"
/db_xref="TAXON:7227"
/clone="BACN37D12"
/clone_lib="DrosBAC1"
/clone_id="pBeloBAC11"
/note="end : SFF6"

ORIGIN

Query Match	29.4%	Score 37;	DB 4;	Length 542;
Best Local Matches	67.5%	Pred. No.	1.5e+02;	
Local Similarity	67.5%	Mismatches	25;	Indels 0;
Matches	52;	Conservative	0;	Gaps 0;
DEFINITION	39 ATTATTAATATACATTTGATTTTATACAGTTTATACTTAACTACATGAGG 98			
LOCUS	49 ATTATTAATATACATTTGATTTTATACAGTTTATACTTAACTACATGAGG 108			
RESULT 10	99 CATAACGGTGGGGGA 115			
LOCUS	109 CTTTTCATGGAAAGGGGA 125			
DEFINITION	CE073145-5 635 bp DNA linear GSS 24-SEB-2003			
ACCESSION	trig-gss-dog-17000323590267 Dog Library Canis familiaris genomic survey sequence.			
VERSION	CE073145			
KEYWORDS	CE073145.1 GI:35136760			
SOURCE	GSS.			
ORGANISM	Canis familiaris (dog)			
REFERENCE	Canis familiaris			
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
1 (bases 1 to 635)				
AUTHORS	Kirkness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.			
TITLE	The dog genome: survey sequencing and comparative analysis			
JOURNAL	Science 301 (5641), 1898-1903 (2003)			
MEDLINE	22875432			
PUBMED	14512627			
COMMENT	Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: skirkness@tigr.org			
FEATURES	Class8: shotgun; Location/Qualifiers			
Source	1. .635 /organism="Canis familiaris" /mol_type="genomic DNA" /strain="Standard Poodle" /db_xref="Taxon:9615" /clone_lib="Dog Library" /note="Site 1: BstXII; Libraries were prepared from peripheral blood"			
ORIGIN	Query Match 29.4% Score 37; DB 9; Length 635; Best Local Matches 64.7% Pred. No. 1.5e+02; Local Similarity 64.7% Mismatches 30; Indels 0; Gaps 0;			
DEFINITION	55; Conservative 0; Libraries were prepared from			
LOCUS	Qy 21 AGAAAAAATCCTGAAAAATTATAATAATACATTTGATTATTATACTATTT 80			
RESULT 11	Db 207 ACATTAATATGATGATGAAATATAAAATTATTTATATAGATT 148			
LOCUS	Qy 81 AATGAGAACTACATGGGCATACGG 105			
DEFINITION	Db 147 ATTATTTATCATGAGACACAG 123			
VERSION	AV207641/c AV207641 RIKEN full-length enriched, adult male testis Mus musculus clone 1700096D08 3', mRNA sequence.			
ACCESSION	AV207641.1 GI:6148494			

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